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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MEMGSNSGPGHGPGQAESGG.....MEDENTRAYDSSSHHTNWSL 375
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1716.686 Million cell updates/sec
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cell division con	serine/threonine	probable GT-like	ecdysone-inducibl	steroid hormone	cnjB protein - T	trfA protein - s	probable C2H2-typ	gene mastermind p	hypothetical pro	BRcore-NS-Z3 prote	1-phosphatidylinos	protein-tyrosine	protein F10A5.24	FTZ-F1 protein -	TOUCH PLONGE

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Qy 1 MEMGSNSGPGHGPGQAESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRV 60	Query Match 99.7%; Score 2033; DB 2; Length 375; Best Local Similarity 99.7%; Pred. No. 6e-146; Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	C;Genetics: A;Gene: spl9; T24P15.11; At2g42200 A;Map position: 2 A;Introns: 120/2; 169/1 C;Keywords: DNA binding; transcription factor	A;Accession: A84851 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-375 <sto> A;Cross-references: GB:AE002093; NID:g2673911; PIDN:AAB88645.1; GSPDB:GN00139</sto>	Nature 402, 761-768, 1999 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197	A;Cross-reterences: EMBL:AJULI038; FID:(ABS05901.1) A;Experimental source: cultivar Columbia; tissue_type inflorescence R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-375 <car></car>	A;Title: Molecular characterisation of the Arabidopsis SBP-box genes. A;Reference number: Z25236; MUID:99453765; PMID:10524240 A;Accession: T52595	A;Cross-references: EMBL:AC002561; NID:g2673901; PID:g2673911 A;Experimental source: cultivar Columbia R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P. Gene 237. 91-104. 1999	A;Accession: T00929 A;Status: translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-375 <rou></rou>	R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul submitted to the EMBL Data Library, December 1997 A;Description: Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence. A;Reference number: Z14212	T00929 T00929 T00929 Squamosa-promoter binding protein 9 [imported] - Arabidopsis thaliana N;Alternate names: transcription factor spl9 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 23-Mar-2001 C;Accession: T00929; T52595; A84851	ALIGNMENTS	36 140 6.9 695 2 T24950 37 129 6.3 1655 2 T13998 38 127 6.2 602 2 F84432 39 126 6.2 1390 2 T14004 40 126 6.2 1748 2 S42136 41 125 6.1 647 2 S04550 42 125 6.1 864 2 A49070 43 124.5 6.1 603 2 F96797 44 123 6.1 1230 2 T18259 45 123.5 6.1 758 2 S45825 46 123.5 6.1 758 2 S45825

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A;Tile: Functional analysis of the Arabidopsis thaliana
A;Reference number: Z24029; MUID:9301089; PMID:9301089
A;Accession: T52593
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R;Cardon, G.H.; Hohmann, S.; Nettesheim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  squamosa promoter binding protein homolog 9 (imported) - Arabidopsis thalian C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
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Keywords: DNA binding; transcription factor
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                                                                                          KGIGDSNCALSLLSNPHQPHD-----NNNNNNNNNNNNTWRASSGFGPMTVTMAQPP
                                                                                                                                          GNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGGTSFSSPEIMDTKLESY
                                                                                                                                                                 GNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGRTSFSSPEIMDTKLESY
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                PAPSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQ
                                                                      KGIGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPP 300
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 PAPSQHQYLNPPWVFKDNDNDMSPVLNLG
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Pred. No. 3.8e-140;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K.; Saedler, H.; Huijser,
 ----QISSGTAMGEFELSDHHHQSRRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 373;
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                                   354
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A; Map position: 3
A; Introns: 105/2; 1
A; Note: T10K17.130
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A;Molecule type: DNA
A;Residues: 1-354 <BEN>
A;Cross-references: EMBL:AL132977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               squamosa promoter-binding protein homolog - Arabidopsis thaliana N;Alternate names: protein T10K17.130 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
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Best Local :
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                                                                                        294 -PPAPSQHQYLNPPWVF----KDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHH
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                       HQSRRQYMEDENTRAYDSSSHHTNWSL 375
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                                                                                                                                                                                                                                                                                                                                                                          RCQVEGCGMDLTNAXGYYSRHRVCGVHSKTFKVTVAGIEQRFCQQCSRFHQLPEFDLEKR
                                                                    QPPISTHQQYLSQTWEVIAGEKSNSHYMSPV---SQISEPADFQISNGTTMGGFELY-LH
                                                                                                                                                                     DSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPM-----TVTMAQP-----
                                                                                                                                                                                                             ----VMQRP---GPWQINPVRETHPHMNVLSHGS----SSFTTCPEMINNNST-----
                                                                                                                                                                                                                                           LDTRYMRRPVSSPSWQINP------MNVFSQGSVGGGRTSFSS-PEIMDTKLESYKGIG
                                                                                                                                                                                                                                                                                   SCRRRLACHNERRRRPOPTT-ALFTSHYSRIAPSLYGNPNAAMIKSVLGD-PTAWSTARS
                                                                                                                                                                                                                                                                                                                   SCRRRLAGHNERRRKPOPASISVLASRYGRIAPSLYENGDAGMNGSFLGNOEIGWPSSRT 192
QQVLKQYMEPENTRAYDSSPQHFNWSL
                                                                                                                                           DSSCALSLLSNSYPIH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204;
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                                                                                                                                         --QQQLQTPTNTWRPSSGFDSMISFSDKVTMAQPPPISTH
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; Pred. No. 9.3e-58;
32; Mismatches 86
 354
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squamosa promoter binding protein-homolog 5 [imported] - garden snapdragon C;Species: Antirrhinum majus (garden snapdragon) (c;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000 C;Accession: T52297 R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijse Gene 237, 91-104, 1999

Huijser,

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A;Title: Molecular characterisation of the Arabidopsis SBP-box genes A;Reference number: Z25236; MUID:99453765; PMID:10524240

A;Reference number: Z25236; A;Accession: T52297 A;Status: preliminary; trans A;Molecule type: mRNA

translated

from

GB/EMBL/DDBJ

RESULT 4 T52297

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squamosa promoter binding protein-homolog 4 [imported] - garden snapdragon (fragment) C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52298
R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P.
Gene 237, 91-104, 1999
A;Title: Molecular characterisation of the Arabidopsis SBP-box genes.
A;Reference number: Z25236; MUID:99453765; PMID:10524240
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A;Cross-references: EMBL;AJ011623; PIDN:CAB56570.1
C;Genetics:
A;Gene: sbph5
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A; Residues: 1-257 < CAR>
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Best Local Similarity
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                                                                                                                                                                                                          25 SSSFSGGLMFGQKIYFEDGGGGSGSSSSSGGRSNRRVRGGGSGQSGQIPRCQVEGCGMDLT
                                                                                                                                                                                                                                                                       Local
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                                                                                                                             SRROYMEDENTRAYDSSSHHTNWSL 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCALSLLSNPHQPHDNNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPP--PAPSQHQYLN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRTLDTRVMRRPVSSPSWQI----NPMNVFSQGSVGGGRTSFSSPEIMDTKLESYKGIGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDLEKRSCRRR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAEESLN---GLKFGKKIYFEEAKAKKGKSTGG-----
                                                                    RRKPQPASLSVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPS-----SRTLDTRV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAGHNERRRKPSPGSM--MSPYYGSLSPTLFDN--QNRTGGFLMDFSTYPNLAGKDSWPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCEVDLSDAKAYYLRHKVCSMHSKSPKVIVAGIEQRFCQQCSRFHQLPEFDQGKRSCRRR 101
 MRRPVSSPSWQINPMNVFSQGSVGGGRTSFSSPEIMDTKLESYKGI-GDSNCALSLLSNP
                                   RRKPPP--VSTISPRYGSLSPTIFDN--YSKPGGFVLDFSSSHPNLTGKDSWANTSSERG
                                                                                                       DAKAYYSRHKVCGMHSKSPKVIVAĞİEQRFCQQCSRFHQLPEFDQGKRSCRRRLAGHNER
                                                                                                                                                                             SSSSLNGLNFGKKIYFEN-VGSSGLQSS----PSKKGRSGGVVQGGQPPRCQVEGCKIDLS
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                                                                                                                                                                                                                                                   127;
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                                                                                                                                                                                                                                                                Score 556; DB 2
Pred. No. 1e-34;
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Pred. No. 4.6e-39;
0; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                        PIDN: CAB56569.1
                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                  DB 2;
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R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, Gene 237, 91-104, 1999
A;Title: Molecular characterisation of the Arabidopsis SBP-box genes.
A;Reference number: 25236; MUID:99453765; PMID:10524240
A;Accession: T52603
                                                                                          squamosa promoter binding protein 2 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C;Accession: T52603
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A; Reference number: Z25236; MUID:99453765; PMID:10524240
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A; Map position:
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A; Residues: 1-425 < CAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, Gene 237, 91-104, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    squamosa promoter binding protein 2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local 9
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                                                                                                                                                                                                                                                                                            QISSGTAMGEFELSDHHHQSRRQYMED
                                                                                                                                                                                                                                                                                                                                   SSSDQPRRFTLDHHP-
                                                                                                                                                                                                                                                                                                                                                                       SSGFGPMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPVLN---
                                                                                                                                                                                                                                                                                                                                                                                                              KTKSARAELFSKEKVTISSHMGASQDLDGALSLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTSFSSPEIMDTK---LESYKGIG-DSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGG---G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FCQQCSRFHCLSEFDEKKRSCRRRLSDHNARRRKPNPGRTYDGKPQVDFVWNRFALIHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FCQQCSRFHQLPEFDLEKRSCRRRLAGHNERRRKPQPA-----SLSVLASRYGRIAPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VKKSKSI----PQRLQTPHCQVEGCNLDLSSAKDYHRKHRICENHSKFPKVVVSGVERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GRSNRRVRGGGSGQSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQR 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGEFAKGIDTSPTLELSFGSGDPVLGLKLGKRTYFEDFWEVENAKGLGLPVSLASSSVSP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGQAESG---GSSTESSSFSG----GLMFGQKIYFED-----GGGGSG-----SSSSG
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binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----WPSSKPVPSRVL---MPQPAKTEISNKLFTEHSRFGLLDP
                                                                                                                                                                                                                                                        -HRNGAGQFNEN 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.6%; Score 400; DB 2; 31.0%; Pred. No. 1.1e-22; tive 51; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                                                            358
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                                                                                                                                                                                                                                                                                                                                   SSNLQPIANRSAAQLSSVSGYWQPDPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                         ---LGRYTEPDNC 331
                                                                                                                                                                                                                                                                                                                                                                                                              ----NSTTW-V
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RESULT 8
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C; Keywords: DNA binding; transcription factor
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A;Cross-references: EMBL:AJ011643; PIDN:CAB56595.1
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                       R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, P. Gene 237, 91-104, 1999
A;Title: Molecular characterisation of the Arabidopsis SBP-box genes.
A;Reference number: Z25236; MUID:99453765; PMID:10524240
A;Accession: T52592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           squamosa-promoter binding protein 6 [imported] - Arabidopsis thaliana
N;Alternate names: transcription factor spl6
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
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A;Map position: 5
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-419 <CAR> A;CODE-references: EMBL;AJ011626; PIDN:CAB56578.1 A;Experimental source: cultivar Columbia; inflorescence
                                                                                                                                                                                                                              A;Gene: spl6
                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.2%;
Best Local Similarity 31.5%;
Matches 116; Conservative 4
                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                        Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: T52592
                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 VKKSKSI-----PQRLQTPHCQVEGCNLDLSSAKDYHRKHRICENHSKFPKVVVSGVERR 208
  62
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                                      QAESGGSSTESSSFSGGLMFGQKIYFE----DGGGGSGSSSSGGRSNRRVRGGGSGQSG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRSNRRVRGGGSGQSGQIPRCQVBGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIBQR 113
EEEDEENISSSSKFSSQEL--NRIDFKLRSFLDLGNDDDDTSSRGFALPSKKSRASNLCS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GEF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOPRRETLDHHPSSNLQPVAHR-----SAAQLNSVSGYWQPDPPAVEGPTAL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FGPMTVTMAQPPPA---PSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAM 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AELFSKEKV---TISSHMGASQDLDGALSLLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTSFSSPEIMDTKLESYKGIG-DSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNNTWRASSG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYENGDAGMNGSFLGNQEIGWPSSRTLDTRV-MRRPVSS--PSWQINPMNVFSQGSVGGG 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGQAESG---GSSTESSSFSG----GLMFGQKIYFED-----GGGGSG------SSSSG 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FCQQCSRFHCLSEFDEKKRSCRRRLSDHNARRRKPNPGRTYDGKPQVDFVWNRFALIHPR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FCQQCSRFHQLPEFDLEKRSCRRRLAGHNERRRKPQPA-----SLSVLASRYGRIAPS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGEFAKGIDTSPSLELSFGSGDPVLGLKLGKRTYFEDFWEVENAKGLGLPVTLASSSVSP 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SEEKFIWPSSKHVPSRVLMPQPAKTEISDTEHNRFGLLDPKTKTAR 314
                                                                                          Conservative
                                                                                      18.4%; Score 374.5; DB 2; 32.4%; Pred. No. 8.4e-21; tive 38; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   %; Score 392; DB 2; Length 41:
%; Pred. No. 4.2e-22;
49; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 419;
                                                                                                                                   Length 405;
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NSTTW-VSSS 352
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                                                                                        77;
                                                                                      Gaps
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                                                                                        14;
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문 4	3	당	Ş	당 성	? ;	문 5	9 1	B 8	문 성	Que Bes Mat	C;Genet A;Gene: C;Keywo		A;Acc	A; Tit	R;Cas	squamo C;Spec C;Date	RESUL T5259	당	Ş	Db	Ş	망	Ş	Дb	Ş	Ф	ঠ	뮍	Ş
60 FYSALSILSTTSDSQGIKHTPVAEPPP 38	HOAHTUTMAGERES A AWTUNNUNNUNNUNNUN HAOOD	GNGSEDQLFTGSTLSFSAFQTSGGFSAGKSNIQLPDKGVGECSGGLHESHD 35	217D 245	3DRROHTSMINNGLSINTRSEEKYTWGTTYETKPTQMESGFTLSFQR 3	AS DELYENGDAGMNGETGNOETGWEEGETTDTEVAMBEDVEGEGWOTNEMNVEG21		05 VTVAGIEORFCOOCSRFHOLPEFDLEKRSCRRRLAGHNERRRKPOPASLSVLASRYGRIA 16	52 SGRSNRVRGGGSQQSQQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPK 104	3 MGSNSGPGHGPGQA-ESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSS 51	17.5%; Score 356; DB 2; Length 396; st Local Similarity 29.4%; Pred. No. 2e-19; ches 103; Conservative 40; Mismatches 97; Indels 110; Gaps 11;	spl10 rds: DNA binding; transcription factor	lduce: 1-396 <car> 1396 <car> 18-references: EMBL:AJO11637; PIDN:CAB56589.1</car></car>	cus: pr	le: Molecular characterisation of the Arabidopsis SBP-box genes. erence number: Z25236; MUID:99453765; PMID:10524240	nann, S.;	protein hambidopsis thaliana (mouse-ear cress) Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000		377 SSHLQRIEQQRNYTGD 392	345 SDHHHQSRQYMED 358	340DYHOMEQPLWIDPGKTNSAGSSSCKGKGTSTVDLLQL 376	FKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEF	288 SSIWDLHETAASRSTRALSLLSAQSQQHLSKFPNTTFSITQPNQNLNHSSST 339	-SNCALSLISNPHQPHDNNNNN	233 SFPGSLLYRVIDEDDHRTSRLVSFKDEPTCSMFPTNEQNSSRTYESKPAIYSTEV 287	SSPEIMDT	180 GKRSCRRLAGHNERRRKPAFYFLPGKRHKLLRTSQDVVGNKFLENSSLVLPE 232	130 EKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPS 189	120 QNPLCQVYGCSKDLSSSKDYHKRHRVCBAHSKTSVVIVNGLEQRFCQQCSRFHFLSEFDD 179	70 QIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDL 129

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squamosa-promoter binding protein 11 [imported] - Arabidopsis thaliana N;Alternate names: transcription factor spl11 (;Species: Arabidopsis thaliana (mouse-ear cress) (;Species: Arabidopsis thaliana (mouse-ear cress) (;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000 C;Accession: T52598 R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijse Gene 237, 91-104, 1999 A;Title: Molecular characterisation of the Arabidopsis SBP-box genes. A;Reference number: Z52336; MUID:99453765; PMID:10524240 A;A;Accession: T52598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein F17L21.14 [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear crees) (c;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 (c;Accession: B8639) (c;Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Anture 408, 816-820, 2000 (cin, C.; Khan, S.; Khaykin, E.; Kim, C.; Khan, S.; Khaykin, E.; Kim, C.; Liu, J.H.; Liu, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, R.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Molecule type: mRNA
A;Residues: 1-393 <CAR>
A;Cross-references: EMBL:AJ011635; PIDN:CAB56587.1
A;Experimental source: cultivar Columbia; tissue_type inflorescence
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A;Gene: F17L21.14
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A; Residues: 1-389 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  T52598
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                                                                                                                       Status: preliminary; translated from GB/EMBL/DDB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMGSNSGPG------HGPGQAESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R-YGRIAPSLYENGDAGMNGSFLG--NOEIGWPSSRTLDTR------WMRRPVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISAVSMKLLTPSVVAGKSKL-----CGQSMPVPRCQIDGCELDLSSAKGYHRKHKVCEK 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DQLVASSSRMFSTSQTSGGFPAGKSKFQLHGEDVGEYSGVLHESQDIHRALSLLSTSSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSWQINPMNVFSQGSVGGGRTSFSSP-EIMDTKLESYKGI----GDSNCALSLLSNPH--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSKCPKVSVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRLSHHNARRRKPQ-GVFSMNPE
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                                                                                                                                                                                                                                                                    S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser,
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C; Genetics:
A; Gene: spll1
A; Map position
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A;Title: Molecular characterisation of the Arabidopsis SBP-box genes
A;Reference number: 225236; MUID:99453765; PMID:10524240
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C;Keywords: DNA binding; transcription factor
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A;Experimental source: cultivar Columbia; tissue_type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
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                                                                                                                                                                                                                                                                Query Match
Best Local (
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                         122 HQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMNGS 178
                                                                                                                                                             121 TGPGSGSGSSYNFLIPKTEVDFTSNRIGLNLGGRTYF----SAADDDFVSRLYRRSRPG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         314 DQLVASSSRMFSTSQTSGGFPAGKSKFQLHGEDVGEYSGVLHESQDIHRALSLLSTSSDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         200 HSKCPKVSVSGLERRFCQQCSRFHAVSEFDEKKRSCRKRLSHINARRRKPQ-GVFSMNPE
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nes 102; Conserv
                                                                                                        64 GSGQSGQI--PRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRF 121
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                                                                                                                                                                                                      7
                                                                              ESGMANSLSTPRCOAEGCNADLSHAKHYHRRHKVCEFHSKASTVVAAGLSQRFCQQCSRF
                                                                                                                                                                                                  SGPGHGPGQAES----GGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRVRGG
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HLLSEFDNGKRSCRKRLADHNRRRKCHQSASATQDTGTGKTTPK--SPNDSGVKAS
                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                16.3%; Score 333; DB 2 41.8%; Pred. No. 9e-18;
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                                                                                                                                                                                                                                            23; Mismatches
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RESULT 13

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unknown protein F14G6.18 [imported] - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) c;Pate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: H96793 C;Accession: H96793 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
T52607
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R;Klein, J.; Saedler, H.; Huijser, P.
Mol. Gen. Genet. 250, 7-16, 1996
A;Title: A new family of DNA binding proteins includes putative transcriptional regulato
A;Reference number: S62360; MUID:96158840; PMID:8569690
A;Accession: S62361
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R;Cardon, G.H.; Hoehmann, S.; Klein, J.; Nettesheim, K.; Saedler, H.; Huijser, Gene 237, 91-104, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         squamosa promoter binding protein 5 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 24-Oct-2000
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A;Residues: 1-171 <KLE>
A;Cross-references: EMBL:X92079; NID:g1183863; PIDN:CAA63061.1; PID:g1183864
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C;Species: Antirrhinum majus (garden snapdragon)
C;Date: 23-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
                                                                                                                             H96793
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A; Residues: 1-181 < CAR >
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A;Accession: T52607
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                                                                                                                                              RESULT 15
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;Keywords: DNA binding; transcription factor
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                                                                                                                                                                                                                        GDSFGE-----GSGRRGFSGQLIQTQE-----RNRVDRKLPMTNSSFK 176
                                                                                                                                                                                                                                                                  ASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRR-PVSSPSWQ 208
                                                                                                                                                                                                                                                                                                                   EVHAKASAATVAGVRQRFCQQCSRFHELPEFDEAKRSCRRRLAGHNERRRK-----IS 138
                                                                                                                                                                                                                                                                                                                                            GVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGSGSSSGGRSNR-----RVRGGGSGQSGQIPR--CQVEGCGMDLTNAKGYYSRHRVC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVEGLMORFCOOCSRFHDLSEFDOTKRSCRRRLAGHNERRRK
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nilarity 63.7%;
Conservative
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43.4%; Pred. No. 7.3e-18;
tive 22; Mismatches 42
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Pred. No. 6.9e-18;
5; Mismatches 28
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       Alonso,
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712
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A;Map position: 1
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A; Residues: 1-1020 <STO>
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Best Local Similarity
Matches 105; Conserv
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                                                                                                                                                                                                                                      211 NMDVMALLTALVCAQGR------NEATTNGS-----PGVPQREQL-LQILNKIKALP
                                                                                                                                                                                                                                                                                 151 ----ASLSVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 RSNRRVR----GGGSGQSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGI 110
                                                                                             NNNNNNNNNTW----RASSGEGPMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPVLN 321
                                                                                                                                                                                         SWQINPMNVFSQGSVGGGRTSFSSPEIMDTKLESYKGIGDSNCALSLLSNPHQPHDNNNN
    LGRYTEPDNCQISSGTAM------
                                                  NSMNGASSPSTMDLLAALSASLG-----SSAPEATAFLSQGGFGNKESNDRT----
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29.7%;
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Pred. No. 7.4e-17;
6; Mismatches 104;
       GEFELSDHHHQSRRQYMEDENTRA
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                                                                                                                                                -NNIGILARKNPEQPSPMNPQ
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.S.; Maiti, R.;
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Search completed: April 10, 2003, 13:54:35
Job time : 23 secs

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Minimum DB
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Listing first 45 s
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Perfect score:
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seq length: 2000000000
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1: /SIDS2/gcgdata/
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| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength		ID	Description
-	2040		- 1	21	AAY70952	Arabidopsis SERK
2	2033	99.7	375	21	AAG31717	
ω	2023	99.2	373	21	AAG31718	
4	2010.5	98.6	378	21	AAG16706	
տ	2000.5	98.1	376	21	AAG16707	
0	1866	91.5	343	21	AAG31719	
7	1843.5	90.4	346	21	AAG16708	Arabidopsis thalia
8	863.5	42.3	350	21	AAG22917	
9	863.5	42.3	354	21	AAG22916	44
10	693	34.0	289	21	AAG22918	

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9WO-EP07				Location 158 /note= "; sequence 242375 /note= ";	ana.	sis rans Bind	interact	st ent		; Prote		262	349	393	2 U	393	389	389	389	376	376	376	405	419	419	419	387	387	336	359	359	440	425	1 L	393	393	393
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				lifiers orresponding codon orresponding codon	-	r Kinase; SERK; v; apomictic seed; tein; SBP; transc	protein #1 from c			375 AA.	ALIGNMENTS	AAG50997	AAB33139	AAG47727	AAG42510	AAG25452	AAG47728	AAG42511 AAG44604	AAG25453	AAG47729	AAG42512	AAG25454	AAU93010 '	AAG48551	AAG48549	AAG48544	AAG48550	AAG48545	AAG50996	AAG50995	AAG19301	AAG14390	AAG44413	AAG12//2	AAG4414	AAG14392	AAG12//3
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				the nucleotide		<pre>ative reproduction; atic embryogenesis; ion factor;</pre>	3A35.					Arabidopsis thalia	Eucalyptus grand	Arabidopsis thal	Arabidopsis thal	Arabidopsis thal	Arabidopsis thal	Arabidopsis thal	Arabidopsis tran	hal	dopsis thal	dopsis t	dopsis thal	dopsis thal	sis thal	dopsis thai	dopsis thal	dopsis thal	sis thal	idopeis thal	idopsis thai	idopsis thal	roopsis char				

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RESULT 2
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Matches 375
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The present amino acid sequence is the SERK-interacting protein #1, isolated from clone 3A35. It is obtained by RT-PCR amplification of early stage Arabidopsis sliquer RN. It is a member of the family of Squamosa-promoter Binding Protein (SBP) transcription factors, after binding of ligand, followed by nuclear translocation of the factors and binding of ligand, followed by nuclear translocation of the factors and binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing vegetative production of a new plant generation through apomixis, comprising transgenically expressing a gene encoding a protein acting in the signal transduction cascade triggered by the Somatic Embryogenesis Receptor Kinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses a plants through seeds ca
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                           AAG31717;
                                                      AAG31717 standard; Protein; 375 AA.
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DB; AAD00300.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPPPPAPSQHQY
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99US-0130479

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netic mapping; gene expression control; promoter;
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 25-FEB-1999
05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
29-MAR-1999
01-APR-1999
                                                                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Local Similarity 98.7%;
les 373; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGGTSFSSPEIMDTKLESY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGGGSGQSGQIPRCQVEGWGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSR
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                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                    thaliana protein fragment
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 99US-0121825.
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Pred. No. 1.8e-173;
0; Mismatches 2;
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RESULT 6
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Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                          Arabidopsis
                                           17-OCT-2000
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Local Similarity 98.7%;
hes 371; Conservative
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                                                                                                                         NTRAYDSSSHHTNWSL
                                                                                                                                                          HQYLNPBWVFKDNDNDMSPVLNLGRYTEDDNCQISSGTAMGEFELSDHHHQSRRQYMEDE
                                                                                                                                                                                                                                        QEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGRTSFSSPEIMDTKLESYKG
                                                                                                                                                                                                                                                                GGSGOSGOI PRCQVEGCGMDLTINAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRFH
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                                                                                                                                                                                            MGSNSGPGHGPGQAESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRVRG
                                                                                                                                                                                                                                QEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGGTSFSSPEIMDTKLESYKG
                                                                              standard;
                          thaliana
                                           (first
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99US-01610815.
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99US-016110980.
99US-0161105.
                                                                              Protein;
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Pred. No. 1.5e-172;
0; Mismatches 2;
                          fragment SEQ
                           ID NO: 38138
                                                                                                                                                                                                                                                                                                                                                                                        21;
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 pathway;
promoter;
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Pred. No. 1.9e-160;
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02-MAR-1999;
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mapping; gene expression control;
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AC ANG22917 standard; Protein, 350 AA. AC ANG22917 AC ANG22917 standard; Protein fragment SEQ ID NO: 26028. XX 17-0CT-2000 (first entry) XX 17-0CT-2000 (first entry) XX Protein identification; signal transduction pathway; metabolic pathway; XX Protein identification; signal transduction pathway; XX Protein identification; signal fransduction pathway; XX Protein identification; signal fransduction pathway; XX Protein identification; signal transduction pathway; XX Protein id	213 NVFSQGSVGGGRTSFSSPEIMDTKLES
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 Score 863.5; DB 21;
Pred. No. 1.1e-69;
                   Length 350;
 RESULT 9
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ID AAG22916
XX AAG2
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05. MAR-1999

09. MAR-1999

23. MAR-1999

23. MAR-1999

25. MAR-1999

01. APR-1999

06. APR-1999

16. APR-1999

16. APR-1999

21. APR-1999

23. APR-1999

23. APR-1999

23. APR-1999

23. APR-1999

24. APR-1999

25. MAY-1999

06. MAY-1999

06. MAY-1999
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GQAESGG-SSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRVRGGGSGQSGQIP
                                                                                                                                                                                            QPPISTHQQYLSQTWEVIAGEKSNSHYMSPV---SQISEPADFQISNGTTMGGFELY-LH
                                                                                                                                                                                                                                                                                                                                                                                                             LDTRYMRRPVSSPSWQINP------MNVFSQGSVGGGRTSFSS-PEIMDTKLESYKGIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCRRRLACHNERRKEOPTT-ALFTSHYSRIAPSLYGNDNAAMIKSVLGD-PTAWSTARS
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                                                                                                        QQVLKQYMEPENTRAYDSSPQHFNWSL 350
                                                                                                                                   HQSRRQYMEDENTRAYDSSSHHTNWSL 375
                                                                                                                                                                                                                                       - PPAPSQHQYLNPPWVF----KDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHH
                                                                                                                                                                                                                                                                                     DSSCALSILISNSYPIH-----QQQLQTPTNTWRPSSGFDSMISFSDKVTMAQPPPISTH
                                                                                                                                                                                                                                                                                                                              DSNCALSLISNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPM-----TVTMAQP-----
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standard; Protein; 354 AA
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(first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 26027.

Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control; termination sequence. pathway; promoter;

Arabidopsis thaliana.

2000EP-0301439 99US-0121825 99US-0123180

99US-012548.
99US-0125788.
99US-0126264.
99US-0126785.
99US-0128714.
99US-0128714.
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99US-0130479.
99US-0130449.
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99US-013048.
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RESULT 10
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CX Arabi
XX Prote
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25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                        Arabidopsis thaliana
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Similarity 52.7%;
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; Pred. No. 1.1e-69;
32; Mismatches 86;
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S-0126264.
S-0126785.
S-0127462.
S-0128234.
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Best Local Sim
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29-OCT-1999
Plant; transcription factor; gene expression; poplar; sweetgum; teak; mahogany; bZIP; G-box
                                                                          AAB33147
                         Eucalyptus
                                          25-JAN-2001
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                                                                                                                                                                                                                  MDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDLEKRSCRRRLAG
                                                                                                                                                                                                 LSNPHQPHDNNNNNNNNNNNNNNNNNNNNNNTWRASSGFGPM-----TVTMAQP------PPAPSQH
                                                                                                                                                                                                                                                            HNERRRKPQPASISVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRR
                                                                                                                    EPENTRAYDSSPOHENWSL
                                                                                                                            EDENTRAYDSSSHHTNWSL
                                                                                                                                                                  OYLNPPWVF----
                                                                                                                                                                                                                                                    QYLSQTWEVIAGEKSNSHYMSPV---SQISEPADFQISNGTTMGGFELY-LHQQVLKQYM
                                                                                                                                                                                     LSNSYPIH----
                                                                                                                                                                                                                                                                                                                             Similarity
                                                                           standard;
                         grandis transcription factor protein sequence #340
                                                                                                                                                                                                                                                                                                                    34.0%;
nilarity 50.8%;
Conservative 3
                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                    9908-0158029

9908-0158029

9908-0159293

9908-0159294

9908-0159292

9908-0159331

9908-0159331

9908-0159637

9908-0159637

9908-0160741

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9908-0160770

9908-016071

9908-016081

9908-016081

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9908-0161406

9908-0161406

9908-0161406

9908-0161359

9908-0161359

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9908-0161359

9908-0161359

9908-0161920

9908-0161920

9908-0161920

9908-0161920
                                                                                                                                                                 -KDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYM
                                                                                                                                                                                   -QQQLQTPTNTWRPSSGFDSMISFSDKVTWAQPPPISTHQPPISTHQ
                                                                            Protein;
                                                                                                                                   375
                                                                                                                                                                                                                                                                                                                  k; Score 693; DB
k; Pred. No. 2.2e
31; Mismatches
                                                                           230
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                                                                                                                                                                                                                                                                                                                             DB 21;
  eucalyptus; pine;
binding factor;
                                                                                                                                                                                                                                                                                                                                    Length
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           acacia;
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99US-0155368.
99US-0156368.
99US-0156368.
99US-0156368.
99US-0156368.

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RESULT 12
AAG12773
ID AAG12
XX
AC AAG12
XX
AC AAG12
XX
DT 17-OC
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Best Local Similarity
                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel plant transcription factors from Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, 'ceak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2 and EREBS, zinc finger domains of type 2 Cyb2His2, CCAAT box elements and MYB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1999;
18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200053724-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
type 2 Cys2His2; CCAAT box element; MYB.
                                                            AAG12773 standard; Protein; 393
                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wood M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eucalyptus grandis.
Arabidopsis thaliana protein fragment SEQ ID NO: 12015
                    17-OCT-2000
                                        AAG12773;
                                                                                                              182
                                                                                                                                  165
                                                                                                                                                       124
                                                                                                                                                                           105
                                                                                                                                                                                               64
                                                                                                                                                                                                                  53
                                                                                                                                                                                                                                                          10 GHGPGQAESGGSSTESSSFSGGLMFGQKIYFED------GGGGSGSSSS----
                                                                                                                                                                                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-579369/54
                                                                                                              SSIFEN--TTRVGSFL 195
                                                                                                                                                VTVAGIEQRFCQQCSRFHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIA 164
                                                                                                                                                                                              PGSGTPPKKVRASAGGGGGGAIQGGQPPRCQVEGCRVDLSDAKAYYSRHKVCGMHSKSAT 123
                                                                                                                                                                                                              --GGRSNRRVR----GGGSG--QSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPK 104
                                                                                                                                  PSLYENGDAGMNGSFL 180
                                                                                                                                                                                                                                      GSGSWTTESGSSSPPPLESLNGLKFGOKIYFQNNNSSNNAAAPKNGSGSGSGSSSAAAPA
                                                                                                                                                                                                                                                                               112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Page 612; 747pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENESIS RES & DEV CORP LTD.
FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McGrath A,
                                                                                                                                                                                                                                                                                                                        230 AA;
                                                                                                                                                                                                                                                                                Conservative
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                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0266513.
99US-0149485.
                                                                                                                                                                                                                                                                              25.2%; Score 514.5; DB 21; 57.1%; Pred. No. 2.3e-38; tive 15; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glenn M;
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                    230;
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termination
                              Protein identification; signal transduction pathway; metabolic pathway; hybridiaation assay; genetic mapping; gene expression control; promoter;
sequence.
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Arabidopsis thaliana

25-FEB-2000; 2000EP-0301439

25-FEB-1999 05-MAR-1999 09-MAR-1999 23-MAR-1999 25-MAR-1999 25-MAR-1999 01-APR-1999 06-APR-1999

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99US-0125788.
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18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 18-JUN-1999 21-JUN-1999 21-JUN-1999

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Matches 121;
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                KTKSARAELFSKEKVTISSHMGASQDLDGALSI
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                                                                                                                                                                        19.7%; ilarity 31.3%; Conservative 5
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99US-0153363

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99US-0153776

99US-0154039

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99US-0161405

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Pred. No. 9e-28;
0; Mismatches 108;
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  -LGRYTEPDNC
                 -NSTTW-V
                                                                                                                                                                          108;
                                                                                                                                                                          Gaps
                                                                              239
                                  279
                                                282
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                                                                                                                            113
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   331
                  323
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17;

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30-JUN

99US-0140353.
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PR 18-JUN-1999 PR 23-JUN-1999 PR 23-JUN-1999 PR 23-JUN-1999 PR 23-JUN-1999 PR 06-JUL-1999 PR 18-JUL-1999 PR 18-JUN-1999 PR 28-JUN-1999 PR 28-	16-JUN- 16-JUN- 17-JUN- 18-JUN- 18-JUN- 18-JUN-
99US-0139457 99US-0139458 99US-0139450 99US-0139451 99US-0139451 99US-0139451 99US-0139452 99US-0140853 99US-0141847 99US-0141847 99US-0142805 99US-0142805 99US-0142805 99US-0142805 99US-0142805 99US-0142805 99US-014384 99US-014384 99US-0144085 99US-0144085 99US-0144085 99US-0144085 99US-0144085 99US-0144085 99US-0145086 99US-0145087 99US-0145087 99US-0145087 99US-0145088 99US-0145087 99US-0145088 99US-0145087 99US-0145088 99US-0145087 99US-0145088 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-0145089 99US-014708 99US-014708 99US-014708 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0147103 99US-0147115 99US-0147115 99US-0147115 99US-0147115	

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65
                13
                                 / Match 19.7%;
Local Similarity 31.3%;
nes 121; Conservative 5
PGEFAKGIDTSPTLELSFGSGDPVLGLKLGKRTYFEDFWEVENAKGLGLPVSLASSSVSP 124
                PGQAESG---GSSTESSSFSG----GLMFGQKIYFED-----GGGGGSG-----SSSSG 53
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99US-015128

99US-016136

                                 50;
                                 Score 401; DB 21;
Pred. No. 9e-28;
0; Mismatches 108;
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31.3%;
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Search completed: April 10, 2003, 13:53:04
Job time: 39 secs

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788.114 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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US-08-317-310A1-15
PCT-US95-13041-2
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US-08-27-033B-43
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APPLICANT: Vertex Pharmaceuticals Incorporated
APPLICANT: Bellon, Steve
TITLE OF INVENTION: Crystallized P38 Complexes
FILE REFERENCE: VPI/98-14
CURRENT APPLICATION NUMBER: US/09/457,040B
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 1584
TYPE: PRT
ORGANISM: DICDI - Dictyostelium Discoideum
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54; Mismatches 153;
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Result No.

Match Query

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152 115.5 Score

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1234 2391 2391 2391 8888 8888 8888 8888 8888 8888 8488 2444 7324 7324 7324 7444 4444 4444 127 127

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461

184

124 213 Minimum Maximum

BB 88

seq length: 0 seq length: 2000000000

Total number

Post-processing:

Database

Title: Perfect score:

US-09-839-185-2 2040 1 MEMGSNSGPGHGP

92:

Copyright

Scoring table: Sequence:

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315 DMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYMEDENTRAYDSSSHHTN 372

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                                                                                                                                                                                                                                                                                                                                                   Query Match 5.7%; Score 115.5; DB 3; Length 591; Best Local Similarity 22.4%; Pred. No. 0.013; Matches 61; Conservative 32; Mismatches 112; Indels 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08965903B Patent No. 6060275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/965,903B
FILING DATE: 07-NOV-1997
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030232
FILING DATE: 07-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R
REGISTRATION NUMBER: 42,995
REFERENCE/DOCKET NUMBER: 8600-0177.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880
TELEPHONE: 650-324-0860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 591 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hacohen, Nir
APPLICANT: Krasnow, Mark A.
TITLE OF INVENTION: SPROUTY PROTEIN AND CODING
TITLE OF INVENTION: SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
180 PPASPVTLAQPRPESERLTNEYVDTPLQHATRSQHPAGQQDNGQTTTHHLLLLPQRNQHL 239
                                                                                            139
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                                                                                                                                                                                                                                                                                                               144 RRRKPQP-----ASLSVLASRYGRIAPSLYENGDA----GMNGSFLGNQEIG-WP 188
                                                                                                                                                                                 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-324-0960
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STATE: CA
                                                                                                                  TKLESYKGIGDSNCALSLLSNPHQPHDNNN--NNNNNNNNNNNTWRASSGFGPMTVTMAQ 292
                                               PPPAPSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEP----DNCQISSGTAM-----GEF 342
                                                                                                                                                                               ASPDFDDYQIHHLTFLPQRPSSLSRNSSTASSTTATGISVSGSGSVSGSSSSFTR----- 138
                                                                                                                                                                                                                          SSRTLD-----TRVMRRPVS-----SPSWQINPMNVFSQGSVGGGRTSFSSPEIMD 234
                                                                                                                                                                                                                                                                    RPRAPEPTLSGVDHTAGATASALASGASSAAPVAIHNNNSQQQLSISAAASNNNTISIIP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
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internal
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COCCOCCCOCCHLCHCCOCCHLCHCCCN COCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Qy 343 ELSDHHHQSR Db 240 HLQOHQQHLQQQ RESULT 3 RESULT 3 US-08-317-310A-15 Sequence 15, Applica Sequence 15, Applica Sequence 15, Applica Facent No. 5859701 FAPPLICANT: WHITE FAPPLICANT: PIERC FAPPLICANT: PIER
W .	EDENTRAYDSSSHTN 3 : : COCCCCCCCCHLOHCCN 2 US/08317310A US/08317310A US/08317310A Tris F. Jian acalyn H. THE IRS FAMILY OF 64 64 5:

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PCT-US95-13041-15
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; FRAGMENT TYPE:
PCT-US95-13041-15
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                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617)227-5941 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US95/13
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/317,310
FILING DATE: 03-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF
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504 DEAAGAA-DLDNR--FRKRTHSAGTSPTISHQKTPSQSSVASIEEYTEMMPAAYPPGGGS 560
                                                                                                                                                              385 VSLSSSSTSGHG-STSDCLFPRRSSASVSGSPSDGGFISSDEYGSSPCDFRSSFRSVTPD 443
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                                                                               444 SLGHTPPARGEEELSNYICMGGKGASTLAAPNGHYILSRGGNGHRYIPGANLGTSPALPG 503
                                    74 CQVEGCGMDLTNAKGYYSRHRVCGV----HSKTP-KVTVAGIEQRFCQQCSRF----- 121
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: JD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Louis Myers
                                                                                                                                                                                                    1 MEMGSNSGPGHGPGQAESGGSSTESSSFSGGLMFGQKIYFEDGG-------
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                                                                                                                                                                                                                                                 104;
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T: SUN, Xiao Jian
T: PIERCE, Jacalyn H.
INVENTION: THE IRS FAMILY OF GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                 1234 amino acids
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                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                  peptide
internal
                                                                                                                                                                                                                                             5.1%; Score 105; DB 5; Length 1234; 21.0%; Pred. No. 0.36; tive 57; Mismatches 176; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT/US95/13041
                                                                                                                     -GGSGSS-----SSGGRSNRRVRGGGSGQSGQIPR
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US-08-446-855A-2
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                                                                                    US-08-446-855A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Stewart
APPLICANT: Flores,
APPLICANT: O'Sulli
                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                    TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Ual-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        TOPOLOGY: 1:
MOLECULE TYPE:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 2391 amino aci
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214 VFSQGS----VGGGRTSFSSPEIMDTKLESY-----KGIGDSNC-ALSLLSNPHQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 614 ----GVAPVPSNRKGNGDY-MPMS-----PKSVSAPQQIINPIRRHPQRVDPNGYMM 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561 GGRLPGYRHSAFVPTHSYPEEGLEMHHLERR-GGHH----RPDTSNLHT-DDGYMPMSP- 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 --PHDNINNNINNNNNNNNTWRASSGFGPMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDM 316
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPEEGARHQHLRLSSSSGRLRYTATAEDSSSSTSSDSLGGGYCGARPESSLTHPHHHVLQ 83
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                                                                                                                                                                    i: 2391 amino acids amino acid
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                                                                                                                                                                                                                                                          703-816-4100
5.1%; Score 105; Di
ilarity 26.2%; Pred. No. 0.9;
Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart,
                                                                                                                       linear
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00 No. 5849573th Glebe Road, 8th Floor
                                                                                                   protein
                                                                                                                                              single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thomas S
                   DB 2;
).93;
                                       Length 2391;
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Matches

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Indels

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Gaps

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CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIËR APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER FILING DATE: 1992-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER APPLICATION NUMBER: 08/446,855
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US-09-150-741-2
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                                                                                                                                                                                                                                                                                                   RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: protein US-09-150-741-2
           TITLE OF INVENTION: Cloning and Expression of a DNA Sequence Encoding Patent No. 6277973

TITLE OF INVENTION: kDa Cryptosporidium parvum Oocyst Wall Protein FILE REFERENCE: 0046.99

CURRENT APPLICATION NUMBER: US/09/451,117

CURRENT FILING DATE: 1999-11-30
                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                 Sequence 2, Application US/09451117 Patent No. 6277973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate Patent No. 6183996
TITLE OF INVENTION: Synthetase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 2, Application US/09150741
Patent No. 6183996
                                                                                                                                              APPLICANT: Jenkins, Mark C. APPLICANT: Fayer, Ronald APPLICANT: Trout, James
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NUMBER OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 GIGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPPPAPSQHQ 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYMEDE-- 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-451-117-2
                                                       ; MOLECULE TYPE: protein US-08-861-464-6
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Best Local Similarity
Matches 34; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,464
FILING DATE: 22-MAY-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/396,001
                                                                                                                                                                                                                                                                                        FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,408
FILING DATE: 16-AUG-1993
ATTORNEY/AGENT INFORMATION:
NUMBE: CITCATOR
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MEDIUM TYPE: Floppy
                                                                                                                                               SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                           NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MI
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OGY: linear
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Austriaco Jr., Nicanor
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5.0%;
26.2%;
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Score 102; DB Pred. No. 0.44;
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                 DB 2;
                     Length 888
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Best Local Similarity

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Best Local (
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tent No.
                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,;
                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/396,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION: Yeast
NUMBER OF SEQUENCES: 16
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                                                                 219
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257 HQPHDNNNNNNNNNNNNTWRASS 281
                               463 HMPLMNSANNKHHGRNNNSMSSHNDND-
                                                                                            404 DNDKAGPNVRMDLINPNLG-PSMQPFHILPPQQNTPPPPWLYSTPPPFNAMVPPHLLAQN 462
                                                                                                                            169 ENGDAGMNGSF-LGNQEIGWPSSRTLDTRVMRRPVSSPSWQIN------PMNVFSQG 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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Cole, Francesca
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                                                              GGGRTSFSSPEIMDTKLESYKGIGDSNC-----ALSLLSNP 256
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26.2%;
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                                                                                                                                                             17; Mismatches
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                                                                                                                                                                                           Score 102;
                                                                                                                                                                              Pred. No. 0.44;
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                               -----NİĞNSNYNNKDTGRSNVGKMKNMKNS 515
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                                                                                                                                                                                          Length 888;
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; SEQ ID NO 6
; LENGTH: 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-323-433A-6
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                                                                                           CURRENT APPLICATION NUMBER: US/09/118,319
CURRENT FILING DATE: 1998-07-17
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Chen, Huizhong
APPLICANT: Ljungdahl, Lars G.
TITLE OF INVENTION: Orpinomyces Cellulase Celf Protein
FILE REFERENCE: 33-98sequence listing
                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09118319 Patent No. 6114158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 0050 1491-003
CURRENT APPLICATION NUMBER: US/09/323,433A
CURRENT FILING DATE: 1999-06-01
PRIOR APPLICATION NUMBER: US 08/396,001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1995-(
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kennedy, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                      ORGANISM: Orpinomyces sp. PC-2 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Saccharomyces cerevisiae
OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
                                                        TYPE: PRT
                                                                          LENGTH: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                516 YHGYYNNNNNNNNNNNNNNNNNSNATN 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      404 DNDKAGENVRMDLINENLG-PSMQPFHILPPQQNTPPPPWLYSTPPPFNAMVPPHLLAQN 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 ENGDAGMNGSF-LGNQEIGWPSSRTLDTRVMRRPVSSPSWQIN--
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Claus, James J
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YEAST
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                                                                                                                                                                                                                and Coding Sequences
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Best Local Similarity

4.9%; 36.1%;

Score 100.5; D Pred. No. 0.22;

DB 3;

Length 432;

Query Match

Matches

22;

Conservative

10;

Mismatches

22;

Indels

7;

Gaps

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PCT-US94-00198-3
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APPLICANT: Schering Corp.
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (201)822-703
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lunn, Paul G.
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: DX:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201)822-7255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,824
FILING DATE: 15-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: 6.0.8
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                 335
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274
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                                                                                                                                                                                                         154 SVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMN 213
                                                                                                              301 TSTSTTAATTKTDADTPSTMNT--
                                                                                                                                            214 VFSQGSVGGGRTSFSSPEIMDTKLESYKGIGDSNCALSLLSNPHQPHDNNNNNNNNNNNN 273
                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino d
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                          ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
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                                               NNIPQRIFSLDDISSFNSSRKSLNLDDSNSLFLWDTSQHSNASMTNTNMHAGVNNSQSQ-
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/ENTION: RAS
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22.0%; Pred. No. 3.3;
tive 30; Mismatches
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                                                                               TWRASS-GEGPMTVTMAQPPPAPSQHQY 302
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                ELSDH-H 348
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APPLICANT: Martin-Heller, Teresa
APPLICANT: Miki L., Brian
TITLE OF INVENTION: NO. 6376747el Plant-Deri
FILE REFERENCE: OB-884280US
CURRENT APPLICATION NUMBER: US/09/384,162
CURRENT FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 6
LENGTH: 286
TYPE: PRT
GRANISN: Dictyostelium discoideum
US-09-384-162-6
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Best Local Similarity
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Patent No. 6376747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

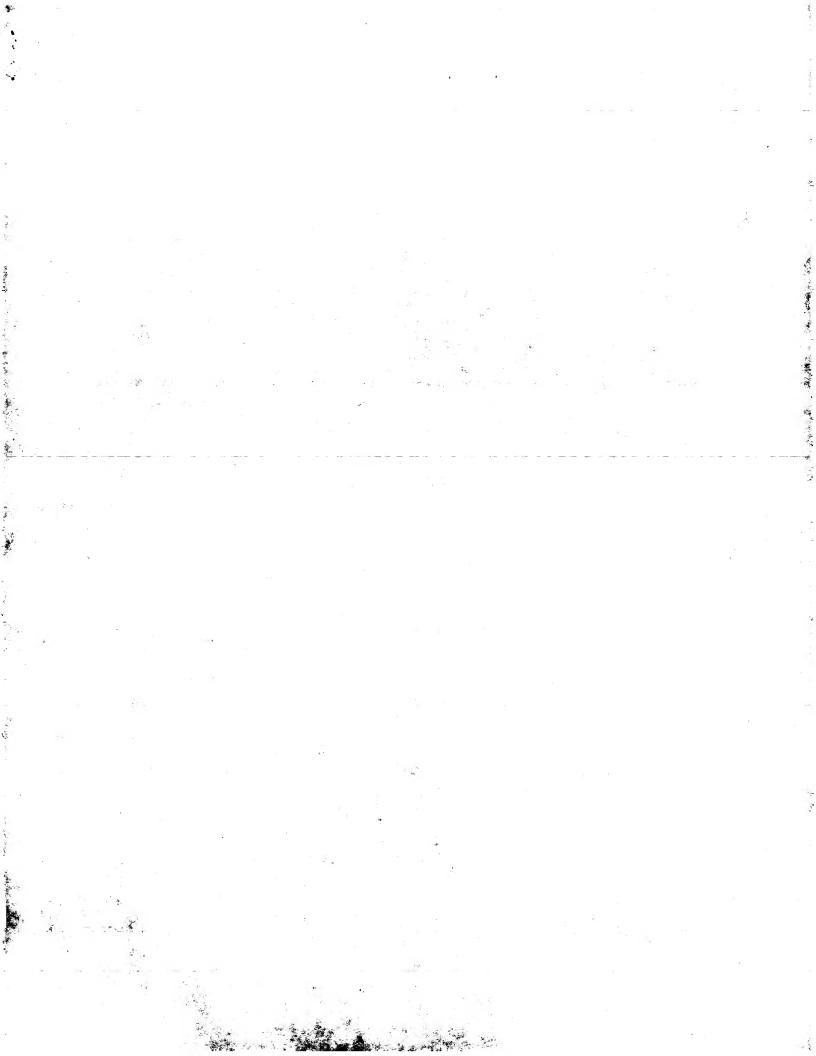
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V/
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/120,817
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APPLICANT: Malik, Kamal
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
FILING DATE: 06-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 GRTSFSSPEIMDTKLESYK-----GIGDSNCALSLL---SN-PHQP------ 259
                 APPLICATION NUMBER: US 6
FILING DATE: 06-AUG-1997
                                                                                                                                                                                                                                                                                                                      STREET:
                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 14603
                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                       CITY: Rochester
                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                      E: Nixon, Hargrave, Devans & P.O. Box 1051, Clinton Square
                                                                                                                                                                                                                                                                                                                                                                                                                                       Alfano, James R
                                                                                                                                                                                                                                                                  U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                HYPERSENSITIVE RESPONSE ELICITOR PSEUDOMONAS SYRINGAE AND ITS USE
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                                      US 60/055,107
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                                                                                                                                                       Version #1.30
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RESULT 15
US-08-914-999-8
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Best Local Similarity
Watches 83; Conserv
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Patent No. 6346406
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein -09-120-817-2
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TELEPAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 LVKSDSDDLKL----ATGNIAMTDVKH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       326 ---TEPDNCQISSGTAMGEFELSDHHHQSRRQYMEDENTRAYD---SSSHHT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268, NNNNNNNTWRASSGFGPMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPV-LNLGRY- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 LSVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPM 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                231 IKVGAGEVFDGHGATFTADKSMGNGDQGENQKPMFELAEGATLKNV-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 -- AGIEQRFCQQCSRF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 TGGGSGGTPTATGGGEGGVTPQITPQLANPNRTSGTGSVS--DTAGSTEQAGKINVVKDT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                STREET: 411 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 RGGGS-----GQSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTV---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                           CITY: Hackensack
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  APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNG-GLGTPSADSGGGGTPDATGGGG---GDTPSATGGGGGDTPTATGGGGGSGGGTPTA 172
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                                                                                                                                                                       New Jersey
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                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                   Ryazanov, Alexey G.
Hait, William N.
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                                                                                                                                                                                                                                                  David A. Jackson,
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                                                                                                                                                                                                                                                                                                          ELONGATION FACTOR-2 KINASE (EF-2 KINASE) AND METHODS OF USE THEREFOR
US/08/914,999
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Continental Plaza,
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Best Local S
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TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Dic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                          168 YENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGRTSF 227
415 NTLNTN 420
                                 367 SSHHTN 372
                                                                         376 --- NNNNNNSSISKSL---
                                                                                                                                                   251 ----SLLSNPHQPHDNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPPPAPSQHQYLNPP 306
                                                                                                                                                                                                                                                                  228 SSPEIMDTKLESYKGIG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 601-1-078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                             WVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYMEDENTRAYDS 366
                                                                                                                                                                                                                             -----DPQIHTYDGVGFGIGNLGQKGFEKFLDTHKCNAICQYLNLQSINPKSEKSDCGT 339
                                                                                                                                                                                                                                                                                                      YNN-----NSGFVSNDERNTPQSFSHFT-----YEHSNHQLLIIDI--QG-VGDHYT-- 285
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 732 amino acids
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21.5%; Pred. No. 0.52;
tive 28; Mismatches
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                                                                       -VEISSGSK----ERNDRDSPSRQLFVSN-----DG 414
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Search completed: April 10, Job time : 19 secs 2003, 13:54:59



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Result
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Maximum Match 100%
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /cgn2 6/ptodata/1/pubpaa/US08
2: /cgn2 6/ptodata/1/pubpaa/PCT N
3: /cgn2_6/ptodata/1/pubpaa/US06_
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/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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Cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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2150
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758
666
824
411
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181
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                           10 US-09-839-185-6
9 US-10-135-322-17
9 US-09-741-233A-2
10 US-09-801-368-132
10 US-09-801-368-36-224
10 US-09-801-368-36-36-224
10 US-09-801-368-312
10 US-09-749-728B-1
10 US-09-749-728B-1
10 US-09-781-693A-2
10 US-09-781-693A-2
10 US-09-832-292-12
10 US-09-832-292-12
10 US-09-832-292-12
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US-09-839-185-4
US-09-819-142-20
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Sequence 2, Appli
Sequence 20, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 6, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 132, App
Sequence 303, App
Sequence 304, App
Sequence 312, Appli
Sequence 36, Appli
Sequence 36720, A
Sequence 17, Appli
Sequence 18, Appli
Sequence 17, Appli
Sequence 55, Appli
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96	96	96.5	97	97	97	97	97.5	97.5	97.5	98.	98	98.5	98.5	98.5	98.5	98.5	98.5	99.5	100	100	100	100	100	100.5	100.5
4.7	4.7	4.7	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9
655	645	724	570	386	251	127	633	440	252	623	623	1331	474	474	474	474	357	861	1207	732	424	424	424	3092	676
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US-09-205-658-57	US-09-919-172-41	US-10-108-605-307	US-09-847-102A-43	US-10-050-704-100	US-09-880-748-1084	US-09-916-940-43	US-10-086-464-11	US-09-932-367A-19	US-09-880-748-1415	US-10-108-605-129	US-10-108-605-125	US-10-087-464-50	US-10-017-754-1812	US-09-849-626-1812	US-09-902-941-1812	US-09-736-457-1812	US-09-864-761-35807	US-09-820-843A-109	US-10-108-605-71	US-09-994-485-8	US-09-879-248-14	US-09-880-371-9	US-09-835-684-9	US-09-801-368-172	US-09-801-368-302
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Sequence 57, Appl	Sequence 41, Appl	Sequence 307, App	Sequence 43, Appl	Sequence 100, App	Sequence 1084, Ap	Sequence 43, Appl	Sequence 11, Appl	Sequence 19, Appl	Sequence 1415, Ap	Sequence 129, App	125,	Sequence 50, Appl	Sequence 1812, Ap	Sequence 1812, Ap	Sequence 1812, Ap	Sequence 1812, Ap	Sequence 35807, A	Sequence 109, App	Sequence 71, Appl	Sequence 8, Appli	14,	Sequence 9, Appli	Sequence 9, Appli	Sequence 172, App	Sequence 302, App

ALIGNMENTS

SEGULT 1
Sequence 2, Application US/09839185
Patent No. US2002069433A1
Patent No. US200206943A1

GENERAL INFORMATION:
APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By Expression of SERK

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Patent Dept.
STREET: 3054 Cornwallis Road
CITY: RTP
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: -Unknown>
AFTORNEY/ACENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO

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RESULT 2
US-09-819-185-4
; Sequence 4, Application US/09839185
; Patent No. US20020069433A1
; GENERAL INFORMATION:
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APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Tinothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: $3,241
REFERENCE/DOCKET NUMBER: $3,241
REFERENCE/DOCKET NUMBER: $3,241
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                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Patent Dept
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                   De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Appomixis Conferred By I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
CLONE: 3A35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schmidt, Eduard Daniel Leendert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYMEDEN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGIGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPPPAPSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KGIGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPMTVTWAQPPPAPSQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGRTSFSSPEIMDTKLESY 240
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                                                                                                                                                                                                                                                                   COUNTRY: US
ZIP: 27709
                                                                                                                                                                                                                                                                                                            STATE: NC
                                                                                                                                                                                                                                                                                                                            CITY: RTP
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Pred. No. le-163;
; Mismatches 0
                                                                                                                                                                           Version
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                                                                                                                                                                                                      ; LENGTH: 138
TYPE: PAT
; ORGANISM: Arabidopsis thaliana
US-09-819-142-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-839-185-4
                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/819,142
CURRENT FILING DATE: 201-03-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09819142 Publication No. US20030041356A1
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reuber, Lynne
APPLICANT: Ratcliffe, Oliver
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Riechmann, Jose Li
APPLICANT: Heard, Jacqueline
                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods for Modifying Flowering FILE REFERENCE: MBI-0033
                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
                                                                                                                                                      Local Similarity
                          97 GVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDLEKRSCRRRLAGHNERRRK 147
                                                                                                    45
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                                                                  29
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86 EVHAKASAATVAGVRORFCOOCSRFHELPEFDEAKRSCRRRLAGHNERRRK 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Arabidopsis thaliana IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVL 156
                                                                  GMDGEEEDGGDEDKRKKVMERVRG---PSTDRVPSRLCQVDRCTVNLTEAKQYYRRHRVC
                                                                                                GGSGSSSSGGRSNR-----RVRGGGSGQSGQIPR--CQVEGCGMDLTNAKGYYSRHRVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDSFGE-----GSGRRGFSGQLIQTQE-----RNRVDRKLPMTNSSFK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRR-PVSSPSWQ 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMDGEEEDGGDEDKRKKVMERVRG----PSTDRVPSRLCQVDRCTVNLTEAKQYYRRHRVC
                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                             Heard, Jacqueline
Adam, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                               Jiang, Cai-Zhong
Riechmann, Jose Luis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 181
                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Suc. No. ...
y 43.4%; Pred. No. ...
-ive 22; Mismatches
                                                                                                                                                      15.8%;
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                                                                                                                                 Score 321.5; DB 7;
Pred. No. 7.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 330; DB 10;
Pred. No. 2.1e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 181;
                                                                                                                                                                      Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 34;
                                                                                                                                        Indels
                                                                                                                                      11,
                                                                                                                                      Gaps
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RESULT 4 US-09-839-185-8

Sequence 8, Application US/09839185 Patent No. US20020069433A1

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Best Local Similarity
Matches 100; Conserv
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TELEPHONE: 919-541-8587
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                             150
                                                                                                                                                                                                                       171
                                                                                                                                                                                                                                                                 110 LQRFCQQCSRFHLLPGFDDGKRSCRRLAGHNKRPRKTNP------------------149
268 IYIDSDDTDVERSPPPTNPATSSLDYPSWIHQSSPPQTSRN------SDSASDQSP 317
                                     267 NINININININTWRASSGEGEMTVTMAQP-----PPAPSQHQYLNPPWVFKDNDNDMSP 318
                                                                                                                                                                                                                                                                                                              111 EQRFCQQCSRFHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYEN 170
                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                           52 LNLNGESDGLFPAKKTKSGAV--CQVENCEADLSKVKDYHRRHKVCEMHSKATSATVGGI 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 ESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSS----GGRSNRR----VRGGGSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornells
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By
Interacting Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
                                                                                                                                                                                                                     GDAGMNGS-----FIGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNV 214
                                                                                                                              ----FSQGSVGGGRTSFSSPE-IMDTKLESYKGIGDSNCALSLLSNPHQPHDNNNNN 266
                                                                                                                                                                           -EPGANGNPSDDHSSNYLLITLLKILSNMH-NHTGDQDLMSHLLKSLVSHAGEQLGKNLV 207
                                                                                                                                                                                                                                                                                                                                                                                                  ------QSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGI 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEGG---EAQQFYGSV------GNSSNSSSSCSDEGNDKKRRAVAIQGDTNGALT 51
                                                                                    ELLLQGRRSQGSLNIGNSALLGIEQAPQEELKQFSARQDGTATENRSEKQVKMNDFDLND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%; Score 306; DB 10; 27.9%; Pred. No. 1.6e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111; Indels 104;
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Sequence 8, Application US/09819142
Publication No. US20030041356A1
GENERAL INFORMATION:
APPLICANT: Reuber, Lynne
APPLICANT: Ratcliffe, Oliver
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Riechmann, Jose Luis
APPLICANT: Heard, Jacqueline
APPLICANT: Adam, Luc
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US-09-819-142-8
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Patent No. US20020069433A1
GENERAL INFORMATION:
APPLICANT: Schmidt, Eduard D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 8
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Best Local
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CURRENT FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: MBI-0033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Methods for Modifying Flowering Phenotypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 RVRG--GGSGQSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQ 116
               APPLICATION NUMBER: US/09/839,185
FILING DATE: 19-Apr-2001
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGIGFRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-30683A
                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC comparible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Patent Dept.
STREET: 3054 Cornwallis Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Schmidt, Eduard Daniel Leendert
De Vries, Sape Cornelis
Hecht, Valerie France Gabrielle
TITLE OF INVENTION: Apomixis Conferred By 1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QCSRFHQLPEFDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QCSRFHDLQEFDEAKRSCRRRLAGHNERRRK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66;
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                                                                                                                                                                                                                                                                                              STATE: NC
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                               CITY: RTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.9%; Score 303.5; DB 9
51.2%; Pred. No. 3.3e-18;
ative 13; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interacting Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -SSGESTYGE-----GSGRRGIN 144
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INFORMATION FOR SEQ ID NO: 6:

CHARACTERISTICS:

TELEPHONE: 919-541-8587

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// TYPE: PRT
// ORGANISM: Arabidopsis thaliana
US-10-135-322-17

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                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                   Matches
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Patent No. US20020173017A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BONKE, AWM
APPLICANT: KAUPPINEN, L
APPLICANT: RIKONEN, M
TITLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND
FILE REFERENCE: 5914-086-999
CURRENT PEPLICATION NUMBER: US/10/135,322
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version SQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BENFEY, PN
APPLICANT: HELARIUTTI
APPLICANT: MAHONEN, I
APPLICANT: BONKE, AWN
                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: 60/253,739
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                           ENGTH: 2150
                                                                                                                                            550
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665
                            258 QPHDNINNNNNNNNNNN 275
                                                                                                        205
                                                                                                                                                                               149 QPASLSVLASRYGRIAPSLYENG----DAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE:
CLONE: 4B19
NSNNNNNNNNNSSNNNNN 682
                                                                                                      P-----SWQINPMNVFSQGSVGGGRTSFSSPEIMDTKLESYKGIGDSNCALSLLSNPH 257
                                                                                                                                          QTISEEILGNK----PVVYNNGNNNNNNNNNNNSTTSNNNITTNNNNNNNNNNNNNNNVLST 604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKOKGKATSSSGV---COVESCTADMSKAKOYHKRHKVCQFHAKAPHVRISGLHORFCQQ 97
                                                                     PRKRTKGNHSKTNSLQDFETSSMNGGDDSISGAGSGGSLRRRNKDDNDENDGNSNNTNSN 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53; Conservative
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MAHONEN, AP
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                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                2000-11-29
                                                                                                                                                                                                               5.9%; Score 121; DB 9;
26.8%; Pred. No. 0.18;
1tive 21; Mismatches 64
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Pred. No. 1.9e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
                                                                                                                                                                                                                   64; Indels
                                                                                                                                                                                                                                                   Length 2150;
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RESULT 8

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CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/09741233A
Patent No. US20020157142A1
GENERAL INFORMATION:
APPLICANT: Glover, Lyn W.
APPLICANT: Budziszewski, Gregory J.
APPLICANT: Zhou, Qing
                                                                                                                                                                                                                                                                                                              GENERAL
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Best Local :
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APPLICANT: Levin, Joshua Z.
TITLE OF INVENTION: Herbicide Target Genes
FILE REFERENCE: PB/5-31127A
                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                   APPLICANT: Busby, APPLICANT: Cali,
                                                                                                                                                APPLICANT:
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                       TITLE OF
                                                                                                        APPLICANT:
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TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                            APPLICANT:
                                                               APPLICANT:
                                                                                     APPLICANT:
                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 NLSFLSGNN--GVTSATSNPNAAAAAAVSSGNLMIS-NHYDGENAVGGGGEGSTGLFPNN 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 SMTRDFLGVGQIVKSMSGSGGFQQQQQQQQQQQQQQQQHGNSRERVGSSSDSADRSSMNVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 NCQ-----AYDSSSHHTN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          409 LMSSADRISSGSVÞSLFSSSMQSPNSAPHMS-ATALLQKAAQMGSTSSNNNNGSNTNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176 NGSFL-GNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGGR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 HHHHHQ-------QGFLAGNNNIKQSPMSFQQNLMQFSHDNHNSAPSNV-----F 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 HFPYGONTNNSNNNTSSMILGLSHMGPPQNLDHQSGDVLRLGSGGGGGGAAS---RSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 CSRFHOLPEFDLEKRSCRRRLAGHNERRRKPOPASLSVLASRYG--RIAPSLYENGDAGM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 HGPGQAESGGSSTESSSFSGGL------MFGQKIYFEDGGGGSGSSSSGGRSNRR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VRGGGSGQSGQIPRCQVEGCGMDL--TNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
ICANT: Summers, Eric
E OF INVENTION: Methods
REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NASSILRSFGSGIYGENESNLQDLMNSFSNPGATGNVNGVD-SPFGSYGGVNKGLSADKQ 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTWRASSGFGPMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPV-----LNLGRYTEPD 329
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                                                                                                                                                               Madden, Kevi
Maxon, Mary
Milne, Todd
                                                                                                                                                                                                          Holtzman, Doug
Madden, Kevin
                                                             Sherman, Amir
Silva, Jeff
                                                                                                 Salama, Sofie
                                                                                                                         Royer, John
                                                                                                                                            No. US20020128250A1man,
                                                                                                                                                                                                                                                  Hecht,
                                                                                                                                                                                                                                                                        Cali, Brian
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                                                                                                                                                                                                                                                                                           Robert
                                                                                                                                                                                                                                              Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.9%; Score 120.5; DB 9; 21.2%; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --SDLIAANASGYFMQEQNPSFH-
                     for Improving Secondary Metabolite Production
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                                                                           ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-303
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                                                                                                                                      NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 303
LENGTH: 1569
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SEQ ID NO 132
LENGTH: 961
                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 303, Application US/10108605 Patent No. US20020160934A1
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    Matches
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/108,605
CURRENT FILING DATE: 2002-03-27
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bachmann, Jane
APPLICANT: Kamdar, Kim
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Broadus, Julie APPLICANT: Stam, Lynn
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/176,418 PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 09/761,142 PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 31133B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDSGSSNGTFNFGESSNEIPTLFRKTNTGSDEN-----VSASGGVRLLDYNSAKPL-- 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPSEL-VSKQKEHKVTFSVENEGLDTRKSSMLGHQTFSCQNS-----LESPLAMYDNK 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPASLSVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQ 208
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72;
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  Conservative
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5.6%; Score 115; DB 9;
20.3%; Pred. No. 0.39;
tive 35; Mismatches 96
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96;
                                       Length 1569;
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  Indels 152;
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                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0
SEQ ID NO 224
LENGTH: 758
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051 NIVIPYSMLAQSKMEIIPYKEIPIPKWRIVDSDNDKGKHSSDESMERKL-----SNGC
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                248 CALSLISNPHOPHDNNNNNN--
                                                549 -----TNPSGQ-NPMINMQPLYQNVSSAMHAFAPQQQFHLPQHYKTNTSVPQ--NDST
                                                                                      196 RVMRRPVSSPSWQINPM-----
                                                                                                                        502 ORMAANOQLONSAFPPDTN-----RIAPA---NNTMPLOPGNMGSPVIENPGMRO---
                                                                                                                                                            136 RRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPSSRTLDT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          992 NSTQQQQNHHGTKINNHHLNGYGDQWGEQSRSRRNSSPSNSHKNERTSERRV-RPIYDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                937 KRQPQHPTGANSSSSLWPDSRQR-----QRQRHHSPSSTSISALSGAKKARKSATNSSSS
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Maxon, Mary
Milne, Todd
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Silva, Jeff
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                                                                                                                                                                                                              5.5%;
                                                                                                                                                                                               22; Mismatches
                                                                                                                                                                                                              Score 112; DB Pred. No. 0.27;
                                                                                    -NVFSQGSVGGGRTSFSSPEIMDTKLESYKGIGDSN 247
                  NNNNNNNTWRASSGFGPMTVTMAQP 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secondary Metabolite Production in Fungi
                                                                                                                                                                                                                                 DB 10;
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                                                                                                                                                                                                                               Length 758;
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CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
VUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
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APPLICANT:
APPLICANT:
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TYPE: PRT
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463 ASAAAGATGTPGTAENVLPVSSMQPLLH-----QANNNSASSATSTAPYPVYSMNVNVPY 517
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                                                                                                                                                                                                                                                                                                                                           NGSFLGNQEIGWP-----SRTLDTRVMRRPVSSPSWQINPMNVFSQG------ 218
                                                                                                                                                                                                                                                                                                                                                                                                                      CSRFHQLPEFDLE--KRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGM 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVEGCGMDLTNAKGYYSRH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVSWSPSRISGKFLIYKELDKENAGSNANATSSGSTDSAVITDGTSGARNNPSSSKIKLP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSSGGRSNRRVRGGGSG-----QSGQIPRC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                         QQQGQISYPFYYTTIPINNPNYYTTQPPNPVTNASTNENQGYSTSSTQHPYYGHPTESQS 462
                                                                                                                                                  NSTTTGN----GPNNINNKSNSSTPLNTVI-----STNNNSANINAAGSNQFTSANK 282
                                                                                                                                                                                                                                                                                                                                                                               IENLHIVSYYSVKDIKONCL-----VTPKASPFLKDVRPSOELIVAMGNTTLGNVKN 234
                                                                                                                                                                                                                                                                ----SVGGGRTSFS----SPEIMDTKLESY------KGIGDSNCALSL 252
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S20020128250A1
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Silva, Jeff
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No. US20020128250Alman,
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Holtzman, Doug
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RESULT 14 US-09-749-728B-1

Sequence 1, Application US/09749728B Patent No. US20020142457A1 GENERAL INFORMATION:

APPLICANT: Umezawa, APPLICANT: Hata, Ji

Akihiro Keiich

APPLICANT: APPLICANT:

Ogawa, Satoshi Hata, Jun-Ichi Fukuda, Keiich

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US-09-801-368-312
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TITLE OF INVENTION: Methods for Improving Se
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 312
LENGTH: 824
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                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                 170 NGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGG-----
339 SHSELDISVYDAAHDH 354
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                                                                                                                                          235 NNQHNQNQHINNNNENT-----
                                                                                                                                                                                                             182 RGKLEVTIIEARDLVTRSKDSQPYVVCT-FESSEFISNGPESLGAINN------NNNNNN
                                                                                                                                                                                                                                                                                                                                              5.3%; Score 109; DB 10; Local Similarity 23.0%; Pred. No. 0.54; les 59; Conservative 31. Minaria.
                                --EDENTRAYDSSSHH 370
                                                                                                     ---VFKDNDNDMSPVLN-LGRYTEPD--NCQISSGTAMGEFELSDH---HHOSRRQYM-
                                                                                                                                                                         NN------NNNNNTWRASSGFGPMTVTMAQPPPAPSQHQYLNPPW-------
                                                                     KKKPLYTHRSSSQLDQLNSCSSVTDPSKRSSNSSSGSSNGPKNDSSHPIWHHKTTFDVLG
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Madden, Kevin
Maxon, Mary
Milne, Todd
No. US20020128250Alman, 7
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Sherman, Amir
Silva, Jeff
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FILE REFERENCE: 00766.000043

CURRENT APPLICATION NUMBER: US/09/749,728B

CURRENT FILING DATE: 2001-09-17

PRIOR APPLICATION NUMBER: HI1-372826

PRIOR FILING DATE: 1999-12-28

PRIOR PRIOR PRICATION NUMBER: FCT-JP00-01148

PRIOR FILING DATE: 2000-02-28

PRIOR FILING DATE: 2000-07741

PRIOR APPLICATION NUMBER: FCT-JP00-07741

PRIOR APPLICATION NUMBER: S00-7740-07741

PRIOR FILING DATE: 2000-11-02

NUMBER OF SEQ ID NOS: 80

SOFTWARE: PATENTIN VEY: 2.0

SEQ ID NO 1

LENGTH: 411
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                                                                                                                                                                                        ; SEQ ID NO 2
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-781-693A-2
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                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/781,693A CURRENT FILING DATE: 2002-07-23 PRIOR APPLICATION NUMBER: US 60/262,312 PRIOR FILING DATE: 2001-01-17 NUMBER OF SEQ ID NOS: 17 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chang, Tai-Jay
TITLE OF INVENTION: ANDROGEN RECEPTOR COMPLEX-ASSOCIATED
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 11709-003001
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TITLE OF INVENTION: THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMY
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 GMNGSFLGNQEIGWPS-SRTLDTR----VMRRPVSS----PSWQI-----NPMNVF 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 5.2%; Score 107; DB 10; Length 411;
Local Similarity 22.8%; Pred. No. 0.33;
hes 64; Conservative 34; Mismatches 111; Indels 7:
                                                                               y Match 5.2%; Score 106; DB 9; Length 860;
Local Similarity 19.8%; Pred. No. 1;
nes 83; Conservative 57; Mismatches 182; Indels 98; Gaps
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5 SNSGPGHGP-GQAESGGSSTESSSFSGGLMFGQXIYFEDGGGGSGSSSSSGGRSNRRVRGG 63
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Search completed: April 10, 2003, 13:55:25 Job time : 25 secs

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Post-processing: Minimum Match 0%
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1 MEMGSNSGPGHGPGQAESGG.....MEDENTRAYDSSSHHTNWSL 375
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	œ	7	6	5	4.	w	2	_	Result No.
356	356	356	365.5	374.5	374.5	392	396	400	417	556	615	863.5	1956	2009.5	2033	Score
17.5	17.5	17.5	17.9	18.4	18.4	19.2	19.4	19.6	20.4	27.3	30.1	42.3	95.9	98.5	99.7	Query Match Length
396	396	392	378	405	394	419	359	425	329	257	323	354	373	374	375	
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	BG
Q8S9L0	Q9ZW53	Q9FZJ9	Q9LQA4	Q9S7A2	Q94JW8	Q9S840	Q9LUF4	Q9SMY0	Q9SM15	Q9SNV4	Q9SNV3	Q9M2Q6	Q9SMX7	Q94AJ2	048527	ID
Q8s9l0 arabidopsis	Q9zw53 arabidopsis	Q9fzj9 arabidopsis		Q9s7a2 arabidopsis	Q94jw8 arabidopsis	Q9s840 arabidopsis		Q9smy0 arabidopsis	Q9sm15 zea mays (n	Q9snv4 antirrhinum	Q9snv3 antirrhinum	Q9m2q6 arabidopsis	Q9smx7 arabidopsis	Q94aj2 arabidopsis	O48527 arabidopsis	Description

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ALIGNMENTS

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"Molecular characterization of the Arabidopsis SBP-box genes."; Gene 237:91-104(1999). EMBL; AC002561; AAB88645.1; EMBL; AJ011640; CAB56592.1;	STRAIN=CV. COLUMBIA; MEDLINE=99453765; PubMed=10524240; Cardon G.H., Hoehmann S., Klein J., Nettesheim K., Saedler H., Huidser P.	(1997).	reargon G.H., Hoenmann S., Netteshelm K., Saequer H., Huljser F.; "Functional analysis of the Arabidopsis thaliana SBP-box gene SPL3: a novel gene involved in the floral transition ".	V. COLUMBIA; 97446501; PubMed=9301089;	RBOM N P	Somerville C.R., Venter J.C.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.	Rounsley S.D., Lin X., Ketchum K.A., Crosby M.L., Brandon R.C., Sykes S.M., Kaul S., Mason T.M., Kerlavage A.R., Adams M.D.,		NCBI_TaxID=3702; [1]	ssicales; Brassicaceae; Arabidopsis.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Rosidae;	Arabidopsis thaliana (Mouse-ear cress).	promoter b	01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	(TrEMBLrel. 06, Created)	048527 PRELIMINARY; PRT; 375 AA.	LT 1 27

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                                                                                                                                                             Yamada K., Liu S.X., Pham P.K., Banh J., Dale J.M., Gibson H.A.,
A Goldsmith A.D., Jiang P.X., Lee J.M., Ondera C.S., Quach H.L.,
A Trang C., Toriumi M., Yu G., Yu S., Bowser L., Carninci P., Chen H.,
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T"Full Length cDNA of gene T24P15.11/At2942200 (GI:2673911).";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
R EMBL, AY046007; AAK76681.1; -
R InterPro; IPR004333; SBP_plant_prot.
R EMBL, SBP, 1.
R SEQUENCE 374 AA, 40733 MW, EA3C1C38200E5386 CRC64;
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Q94AJ2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative squamosa-promoter-binding protein.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 2.6e
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Pred. No. 3.5e-153;
D; Mismatches 1;
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                                                     .6e-151;
es 2;
                                                                                                           DB 10; Length 374;
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Best Local
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01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cardon G.H., Hoehmann S., Nettesheim K., Saedler H., Huijser I "Functional analysis of the Arabidopsis thaliana SBP-box gene novel gene involved in the floral transition."; Plant J. 12:367-377(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. LANDSBERG ERECTA; TISSUE=FLOWER; MEDLINE=97446501; PubMed=9301089;
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                   Gene 237:91-104(1999).
EMBL; AJ011639; CAB56591.1;
                                                                                                                                                                                                                                                                                                                                                                                                                           Huijser
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cardon G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CV. LANDSBERG ERECTA; TISSUE-FLOWER; MEDLINE=99453765; PubMed=10524240;
                                                                                                                                                                                                                                                                                                     Pfam; PF03110; SBP; :
                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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RGGGSGQSGQIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSR
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000 (TrEMBLrel. 13, Last sequence update)
002 (TrEMBLrel. 21, Last annotation updat
promoter binding protein-like 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FROM N.A.
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                                                                                                                                                                            Conservative
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96.1%;
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0; Mismatches
                                                                                                                                                                                                   Score 1956; DB 10;
Pred. No. 4.4e-147;
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Benes V., Wurmbach E., Drzonek H., Ansorge W.,
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Mayer K.F.X. (NOV-1999) to the EMBL/GenBank/DDBJ
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T10K17.130.

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AL132977; CAB67620.1; -
InterPro; IPR004333; SBP plant prot.
Pfam; PF03110; SBP; 1.
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Best Local Similarity
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Squamosa promoter binding protein-homologue 5 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03110; SBP;
NON TER 1
SEQUENCE 323 AA;
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EMBL; AJ011623; CAB56570.1; -.
InterPro; IPR004333; SBP_plant_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antirhinum majus (Garden snapdragon).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; euasterids I; Lamiales; Veronicace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99453765; PubMed=10524240; Cardon G.H., Hoehmann S., Klein J.,
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PPWVFKDN--DN---DMSPVLNLGRYT---
                                                                                                                  NCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPMTVTMAQPP---PAPSQHQYLN
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                                                                        STALSLLSN--QSWGSRNSNNFLGTNGN
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Pred. No. 6.5e-41;
0; Mismatches 91;
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RESULT
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Matches 127
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Q9SNV4;
Q1-MAY-2000
Q9SM15;
Q9SM15;
01-MAY-2000
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Squamosa promoter binding protein-homologue 4 (Fragment).
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Veronicaceae; Antirrhinum.
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Cardon G.H., Hoehmann S., Klein J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSSSLNGLNFGKKIYFEN-VGSSGLQSS---PSKKGRSGGVVQGGQPPRCQVEGCKIDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRVRGGGSGQSGQIPRCQVEGCGMDLT 84
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Pro; IPR004333; SBP_pla
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Similarity 49.4%;
27; Conservative 37
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  Created)
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Pred. No. 2.3e-36;
7; Mismatches 73;
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SBP-box gene SPL3:
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Best Local :
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Q9SMY0,
Q9SMY0,
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
7-7-7-7-7-7-8 promoter binding protein-like 2.
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STRAIN=CV. T232; TISSUE=EARLY FEMALE INFLORESCENC STRAILNECY T232; TISSUE=EARLY FEMALE INFLORESCENC MEDLINE=97446501; PubMed=9301089;
Cardon G.H., Hoehmann S., Nettesheim K., Saedler "Functional analysis of the Arabidopsis thaliana novel gene involved in the floral transition.";
Plant J. 12:367-377(1997).
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam;
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Spermatophyta; Magnoliophyta; Li
Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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EMBL; AJ011618; CAB56631.1;
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Pfam; PF03110; SBP; 1.
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                                                                                                                                                                                                              337
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                                                                                                                                                                                                                                                                                                                                                                                                          RSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMNGSFL-----
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                                                                                                                                                                                                                                                  TVTMAQPPPAAS---QHQYLNP-PWVFKDNDNDMSPVLNLGR----YTEPDNC---QISSG
                                                                                                                                                                                                                                                                                                                                                                                    KSCRKRLAGHNERRRRPPPGP---LASRYGRHAASL---
                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSHHGQFSGELELALQGNRPAPGSAAPPAPRNNQGSAGT--FDQAGNTMDWSL
                                                                                                                                                                                                             TA-----MGEFELSDHHHQ------SRRQYMEDENTRAYDSSSHHTNWSL 375
                                                                                                                                                                                                                                                                                                    MRGGFPAVRPGGERV----PGGIQWQAGLDPRH--HQGAVAGYGAHYGSEGGSSSSARPP
                                                                                                                                                                                                                                                                                      VFPGPELPPGGCLAGVPADSSCALSLLST--QPWDAAHSHSHSHA-----APTAGFD--
                                                                                                                                                                                                                                                                                                                                                             QEIGWPSSRTLDTRVMRRPVSSPSWQ--INPMNVFSQGSV------
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                                                                                                                                                                                                                                       GGSPVAPSLMAASSYIAPSPWTETDSWGHEG----
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yta; Liliopsida;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 417;
Pred. No. 3.
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annotation update)
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a; Poales; Poaceae; PACC clade;
   Arabidopsis
              Embryophyta;
edons; core eu
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).2e-25;
les 97;
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              a; Tracheophyta;
eudicots; Rosid
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Best Local S
Matches 120
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Q9LUF4;
Q9LUF4;
Q9LUF4;
Q9LUF4;
Q9LUF4;
Q9LUF4
Q9LUF4
Q9LUF4;
Q1-OCT-2000 (TrEMBLrel. 15, Created)
Q1-OCT-2000 (TrEMBLrel. 21; Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21; Last annotation update)
Similarity to squamosa promoter binding protein.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
  STRAIN=COLUMBIA;
MEDLINE=20181125;
Sato S., Nakamura
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cardon G.H., Hoehmann S., Nettesheim K., Saedler "Functional analysis of the Arabidopsis thaliana novel gene involved in the floral transition."; Plant J. 12:367-377(1997).
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                                                                          SEQUENCE FROM N.A.
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; AJ011625; CAB56577.1;
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NCE 425
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PubMed=10718197;
Y., Kaneko T., K
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     Katoh
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     Asamizu
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     Kotani H.,
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01-MAY-2000
01-MAY-2000
01-JUN-2002
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SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA; TISSUE=INFLORESCENCE;
MEDLINE=99453765; PubMed=10524240;
                                                                                           Cardon G.H., Hoehmann S., Ne "Functional analysis of the novel gene involved in the f plant J. 12:367-377(1997).
                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA; TISSUE=INFLORESCENCE;
MEDLINE=97446501; PubMed=9301089;
                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                            NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interPro; IPR004333; SBP_plant_prot.
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AB025619; BAB09142.1;
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promoter binding protein-like 2.
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39108 MW;
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                                                                                                                 Nettesheim K., Saedler he Arabidopsis thaliana le floral transition.";
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Similar to squamosa-promoter
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                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosic
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AJ011626; CAB56578.1; -.

EMBL; AJ011624; CAB56576.1; -.

EMBL; AB017070; BAB10590.1; -.

InterPro; IPR004333; SBP_plant_prot.
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                                                       SEQUENCE FROM N.
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01-JUN-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Squamosa promoter binding protein-like 6.
SPL6 OR F23010.24.
Arabidar-1-
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            Gene
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Q9S7A2;
                                                            MEDLINE=99453765; PubMed=10524240; MEDLINE=99453765; PubMed=10524240; MEDLINE=99453765; Mechmann S., Klein J.,
                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabic
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Pfam; PF03110; SBP; 1.
                                                                                                                             Cardon G.H., Hoehmann S., Nettesheim K., Saedler "Punctional analysis of the Arabidopsis thaliana novel gene involved in the floral transition."; Plant J. 12:367-377(1997).
                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA;
MEDLINE=97446501; PubMed=9301089;
Cardon G.H., Hoehmann S., Nettesh
                                                  Huijser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKRSCRRRLAGHNERRRK---PAFYFLPGKRH-----KLLRTSQDVVGNKFLENSSLVLPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAGMNGSFLGNQEIGWPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QIPRCQVEGCGMDLTNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEEDEENISSSSKFSSQEL--NRIDFKLRSFLDLGNDDDDTSSRGFALPSKKSRASNLCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAESGGSSTESSSFSGGLMFGQKIYFE-----DGGGGSGSSSSGGRSNRRVRGGGSGQSG
                          237:91-104(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDH - - HHOSRROYMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSIWDLHETAASRSTRALSLLSAQSQQHLSKFPNTTFSITQPNQNLNHSSST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESYKGIGD----SNCALSLISNPHQPHDNNNNN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFPGSLLYRVIDEDDHRTSRLVSFKDEPTCSMFPTN--EQNS---SRTYESKPATYSTEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                    FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -RTLDTRVMR--RPVS---SPSWQINPMNVFSQGSVGGGRTSFSSPEIMDTKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358
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                                        of,
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                                        Arabidopsis
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                                                                                                                                                                                                                                               Arabidopsis
                                                                                                                                                                                                                                                                       Embryophyta;
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                                        SBP-box
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                                                                                                                                                        H., Huij
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                                                                                                                                                                                                                                                              eudicots;
                                                                 Saedler H.,
                                                                                                                                                                                                                                                                           Tracheophyta;
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                                        genes.";
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Q9LQA

ID Q94

AC Q9LQA

AC Q9LQA

DT 01-OC

DT 01-UC

DT 01-UC

DE F4NZ.

OS Arabi

OC Eukas

OC Sperm

OC Sperm

OC SPERM

OC SPERM

OC HUTOS

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RN Shipul

RA Huiza

RA Pedes

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Best Local Sim
Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LQA4
Q9LQA4;
01-OCT-2000
                                                                                                                                                                                          Shinn P., Brooks S., Buehler E., Chao Q., Dunn P., Khan S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Han Huizar L., Kremenetskaia I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V., Yu G., D., Federspiel N.A., Theologis A., Ecker J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2001) to the EMBL/GenBank/DDBJ EMBL; AJ011644; CAB56596.1; -. EMBL; AJ011643; CAB56595.1; -. EMBL; AC018364; AAG52487.1; -. Interpro; IPR004333; SBP_plant_prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thallana chromosome 1 BAC F23010 genomic sequence."; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                Submitted (OCT-2000) to the EMBL/GenBank/DDBJ EMBL; AC008262; AAF27058.1; -.
                             Pfam;
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
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  SEQUENCE
                          InterPro; IPR004333; SBP_plant_prot.
Pfam; PF03110; SBP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEEDEENISSSSKFSSQEL--NRIDFKLRSFLDLGNDDDDTSSRGFALPSKKSRASNLCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESYKGIGD-----SNCALSLLSNPHQPHDNNNNN------NNNNNNNNTWRASSGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFPGSLLYRVIDEDDHRTSRLVSFKDEPTCSMFPTN--EQNS---SRTYESKPAIYSTEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-----RTLDTRVMR--RPVS---SPSWQINPMVVFSQGSVGGGRTSFSSPEIMDTKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
SBP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -DYHQMEQPLWIDPGKTNSAG
                                                                                                                                                                     for Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45952 MW; B7DD1356C6DEE259 CRC64;
  42923 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 9.8e-22;
  OEF6AC58D7C0DF49 CRC64;
                                                                                                                                                                   BAC
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                                                                                                                databases
                                                                                                                                                                     F4N2 from
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                                                                                                                                                                                                                                                                                Hansen
                                                                                                                                                                                                                           Davis R.W
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01-JUN-2002
F17L21.15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Q9ZW53;
01-MAY-1999 (TrEMBLrel. 1
01-MAY-1999 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO0455; AAF99748.1;
InterPro, IPRO04333; SBP_plant_prot.
Pfam; PF03110; SBP; 1.
SEQUENCE 392 AA; 43695 MW; 014C50C312111AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid:
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI TaxID=3702;
STRAIN=CV. COLUMB:
MEDLINE=99453765;
Cardon G.H., Hoehr
                                                                                                                                               Cardon G.H., Hoehmann S., Nettesheim K., Saedler "Functional analysis of the Arabidopsis thaliana novel gene involved in the floral transition.", plant J. 12:367-377(1997).
                                                                                                                                                                                                                                                           STRAIN=CV. COLUMBIA; TISSUE=FLOWE MEDLINE=97446501; PubMed=9301089;
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STRAIN=CV. COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFS-----
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     PubMed=10524240;
mann S., Klein J.,
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                                                              TISSUE-FLOWER;
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Last annotation update)
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Pred. No. 2.7e-20;
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     Nettesheim K.,
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     Saedler H.,
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"Molecular Characterization of ti
Gene 237:91-104(1999).
EMBL; AJ011637; CAB56589.1; -.
EMBL; AJ011636; CAB56588.1; -.
InterPro; IPR004313; SBP plant p
Pfam; PF03110; SBP; 1.
rch completed: April
time : 37 secs
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                                                                                                             GNGSEDQLFTGSTLSFSAFQTSGGFSAGKSNIQLPD-
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              2003, 13:54:07
                                                                                                                                        -QGSVGGGRTSFSSPEIMDTKLESYKGIG----
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                                                        -TSDSQGIKHTPVAEPPP
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Q04003 zea mays (m
Q38741 antirrhinum
P33244 drosophila
Q91qz7 arabidopsis
P18160 dictyosteli
P54674 dictyosteli
P13054 drosophila
                                                                                                          P54675
Q02199
Q021380
O14429
O22299
Q92259
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Q92212
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Q24432 drosophila
P36168 saccharomy
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61

Query Match Best Local : Matches

65;

Conservative

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Score 330; DB 1; Length 171; Pred. No. 4.4e-17; Mismatches 28; Indels

4

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Similarity

16.2%; 63.7%;

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004003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moreno M.A., Harper L.C., Krueger R.W., Dellaporta S.L., Freeling M. Liguleless encodes a nuclear-localized protein required for induction of ligules and auricles during maize leaf organogenesis.", Genes Dev. 11:616-628(1997).

-I- FUNCTION: INVOLVED IN THE FORMATION OF LIGULES AND AURICLES DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               Nuclear protein; Developmental protein.

DOMAIN 243 259 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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Pfam; PF03110; SBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U89496; AAB51071.1; -
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                                                                                                                                                                                                                                                                                                                        Local
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TISSUE SPECIFICITY: LEAF LIGULAR REGION, BLADE AND
DEVELOPMENTAL STAGE: DEVELOPING LEAVES. PRESENT AT
LEVELS IN VERY YOUNG LIGULES AND AURICLES. PRESENT
LIGULE AND AURICLE DEVELOPMENT.
SIMILARITY: CONTAINS 1 SBP DOMAIN.
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                                                         ALLSKEQDQTMDLGEVVKEAVDPKGKASMQQHYGFPFHSSSAGSCFPQTQAVSS
                                                                                                                                               RRRLAGHNERRRKPQP------ASLSVLASRYGRIAPSLYENGDAGMNGSPLGN
                                                                                                                                                                                  AEGCKADLSSAKRYHRRHKVCEHHSKAPVVVTAGGLHORFCOQCSRFHLLDEFDDAKKSC 246
                                                                                                                                                                                                                                              SSAEENMASFAATQLGLNLGYRTYFPPRGGYT------
                              KLESYKGIGDSNCALSLLSNP----HQPHDNNN
                                                                                     QEIGWPSSRTLDTRVMRRPVSSPSWQIN-----
                                                                                                                       {\tt RKRLADHNRRRKSKPSDADAGDKKRAHANKAAAAKDKAESSSKNMDIGD-GLGAQILGS}
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399 AA;
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31.4%; Pred. No. 3.9;
tive 32; Mismatches
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Q38741;
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                                                                                                                                                                                          Nuclear hormone receptor FTZ-F1 (FTZ-F1 alpha) FTZ-F1 OR NR5A3.
                                                                                                                                                                                                                                                                                                                                                                                             DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X92369; CAA63113.1; -.
InterPro; IPR004333; SBP_plant_prot.
Pfam; PF03110; SBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein J., Saedler H., Huijser P.; "A new family of DNA binding proteins includes putative transcriptional regulators of the Antirrhinum majus flo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence up.
15-JUL-1999 (Rel. 38, Last annotation.
Squamosa-promoter binding protein 1.
                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; DNA-binding; Nuclear protein.

DOMAIN 52 126 SBP.

SEQUENCE 131 AA; 14919 MW; 71DA57E150E4B23C CRC64;
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Klein J., Saedler H., Huijser P.;
                                           NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                      P33244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Nuclear.-!- SIMILARITY: CONTAINS 1 SBP DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identity gene SQUAMOSA."
Mol. Gen. Genet. 250:7-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF THE SQUAMOSA GENE.
                                                                                                                                                                                                                                                                                                                                                                      DROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FHAKAPVVLHSGLQQRFCQQCSRFHELSEFDEAKRSCRRRLAGHNERRRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSQEQGEEEDDIGEDSKKTRALTPSGKRASGSTQRSCQVENCAAEMTNAKPYHRRHKVCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60;
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                                                                                                                                                                                                                                                 (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 38, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GRSNRRVRG---GGSGQSGQIPR-CQVEGCGMDLTNAKGYYSRHRVCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250:7-16(1996)
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54.5%;
PARTIAL
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Pred. No. 2
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  SEQUENCE
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SEQUENCE

FROM N.A.,

AND

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Pfam; PF00104; hormone rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDPINGER.
ProDom; PD000035; Znf C4steroid;
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnP_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     homeodomain protein Ftz.";
Nature 385:552-555(1997).
-!- FUNCTION: ACTS AS A CO
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Yu Y., Li W., Su K., Yussa M., Han W.,
"The nuclear hormone receptor ftz-f1 i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ptz are mutually dependent cofactors.";
Nature 385:548-552(1997).
[5]
CHARACTERIZATION.
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Guichet A., Copeland J.W.R., Erdelyi M., Hlousek D., Zavorszky
Ho J., Brown S., Percival-Smith A., Krause H.M., Ephrussi A.;
"The nuclear receptor homologue Ftz-F1 and the homeodomain prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weda H., Sun G.-C., Murata T., Hirose S.; 
"A novel DNA-binding motif abuts the zinc 
nuclear hormone receptor FTZ-F1 and mouse 
repeat-binding protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lavorgna G., Ueda H., Clos J., Wu C.; "FTZ-F1, a steroid hormone receptor-like activation of fushi tarazu.";
                                                                                                                                                                                                                                                                                           FlyBase; FBgn0001078; ftz-f1.
InterPro; IPR000536; Hormone_rec_lig.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M63711; AAA28542.1;
HSSP; P19793; 2NLL.
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                                                 PROSITE; PS00031; NUCLEAR RECEPTOR; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION.
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                            Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE BINDING OF FTZ TO DNA. BINDS THE SEQUENCE ELEMENT 5'.

YCYCGYCR-3' IN THE ZEBERA BLEMENT OF TZ. PROBABLY ALSO FUNCTION

AS A RECEPTOR FOR A YET UNKNOWN LIGAND.

AS A RECEPTOR FOR A YET UNKNOWN LIGAND.

SUBUNIT: WONOMER; FORMS A COMPLEX WITH FTZ.

SUBCELLULAR LOCATION: Nuclear.

TISSUE SPECIFICITY: EXPRESSION IN THE PARASEGMENTAL PRIMORDIA OF THE EMBRYONIC BLASTODERM.

OF THE EMBRYONIC BLASTODERM.

DEVELOPMENTAL STAGE: FIRST APPEARS IN BLASTODERM EMBRYOS. IT IS ABSENT IN SUBSEQUENT EMBRYO STAGES, AND THEN REAPPEARS IN LATE EMBRYOGENESIS TO BE FOUND IN LARVAE, PUPAE AND ADULTS.

NEMEROPERATOR OF THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C.K., Ueda H., Petkovich M.;
Drosophila nuclear receptors FTZ-F1 a
ete as monomers for binding to a site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell. Biol. 14:3166-3175(1994).
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GLN-RICH
                                                 1.
DNA-binding; Nuclear
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e in the fushi tarazu
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Bearing Constitution of

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Matches 91
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SEQUENCE
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DOMAIN
SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE-21016719; PubMed=11130712;
Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks
Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dev
                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Zinc finger protein constans-like 6.
ATIG75540 OR F10A5.24
                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                     Spermatophyta; Magnoliophyta; eurosids II; Brassicales; Bras
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91; Conservative
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24.7%;
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                                                                                                      Brassicaceae;
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C-SS: 100-FOLD LESS BINDING.

R-QO: 100-FOLD LESS BINDING.

R-SO: 100-FOLD LESS BINDING.

M-SI: 10-FOLD LESS BINDING.

M-SI: 10-FOLD LESS BINDING.

GG->AA: NO BINDING.

GG->AA: NO BINDING.

R-SO: 10-FOLD LESS REDUCED BII

R-SO: 10-FOLD LESS REDUCED BII

R-SO: 10-FOLD LESS REDUCED BII
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Pred. No. 0.0
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D: NO EFFECT ON BINDING.
0C4539F944921617 CRC64;
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DT 01-NOV-1990
DT 01-OCT-1996
DT 15-JUN-2002
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Best Local
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InterPro; IPR000315; Znf Bbox.
InterPro; IPR007926; Znf Constans.
Pfam; PF00643; Zf-Bbox; 2.
ProDom; PD007661; Znf Constans; 2.
SMART; SM00336; BBOX; 2.
PROSITE; PS50119; ZF-BBOX; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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DOMAIN
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SIMILARITY: BELONGS TO THE CONSTANS FAMILY.
SIMILARITY: CONTAINS 2 B BOX-TYPE ZINC FING
                                                                                                                                                                                                                                                                                                                                                                                APSLYENGDAGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGG-
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                                                                                                                                                                                 LNLGRYTEPDNCQISSGTAMGEFELSDHHHQSRRQYMEDENTRAYD
                                                                                                                                                                                                                                                N---NNNNNNNNNTWR-ASSGFGPMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPV
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ear_protein; Repeat; Multi;
47
B BOX-TYPE 1.
102
B BOX-TYPE 2.
126
POLY-SER.
238
POLY-ASN.
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Pred. No. 0.
                                                                  PRT;
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   Pfam; PF00069; pkinase; I

Pfam; PF00536; SAN; 1.

Pfam; PF00622; SPRY; 3.

ProDom; PD000001; Euk pki

SMART; SM00454; SAN; 1.

SMART; SM00449; SPRY; 3.

SMART; SM00221; STYKC; 1.
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InterPro; IPR000719; Euk
InterPro; IPR001660; SPR
InterPro; IPR003878; SPR
InterPro; IPR003877; SPR
InterPro; IPR004040; STY
InterPro; IPR001245; Tyr
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DOMAIN 9
DOMAIN 4
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Nuckolls G.H., Osherov N., Loomis W.F., Spudich J.A.;
"The Dictyostelium dual-specificity kinase splA is ess
spore differentiation.";
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MEDLINE=90287147; PubMed=1972546;
Tan J.L., Spudich J.A.;
"Developmentally regulated protein-tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYKA OR SPLA OR I
                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN KINASE ATP; PROSITE; PS00111; PROTEIN KINASE DOM; PROSITE; PS00109; PROTEIN KINASE TYR; PROSITE; PS50105; SAM_DOMĀIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M33785; AAA33: PIR; A35670; A35670
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403
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808
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11215
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   480
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1233
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STY_pkinase.
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Dictyosteliida; Dictyostelium
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POLY-THR.
POLY-ASN.
POLY-ASN.
POLY-ASN.
POLY-ASN.
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(EC 2.7.1.112) (Tyrosine-

essential

genes ij

FUNCTION: ESSENTIAL FOR SPORE DIFFERENTIATION. CATALYTIC ACTIVITY: ATP + a protein tyrosine = D ADP + protein

PROTEIN KINASES

between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U entities requires a license agreement (See This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and There are no restrictions ng as its content is in http://www.isb-sib Usage and the through and yh a collaboration EMBL outstation for .ch/announce, 9 9

ATP-binding; Phosphorylation

European Bioinformatics Institute.

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01-OCT-1996
01-OCT-1996
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NP_BIND

BINDING

ACT_SITE

CONFLICT

CONFLICT

SEQUENCE
                                                 MEDLINE-96009592; PubMed=7565716;
Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
Zhou K., Takegawa K., Emr S.D., Firtel R.A.;
"A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: biological roles of putative mammalian pl10 and yeast vps34p PI 3-kinase homologs during growth and development.";
MO1. Cell. Biol. 15:5645-5656 (1995).
-i- CATALYTIC ACTIVITY: ATP + 1-phosphatidyl-1D-myo-inositol = AI
1-phosphatidyl-1D-myo-inositol 3-phosphate.
                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Phosphatidylinositol 3-kinase 2 (BC 2.7.1.137)
(Ptdlns-3-kinase) (PI3K).
                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        PIKB OR PIK2
                                                                                                                                                                                                                                                                                                                                                     P3K2_DICDI
             This SWISS-PROT entry is copyright.
                                          -!- SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                           462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402
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                                                                                                                                                                                                             TaxID=44689;
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97; Conserv
  the Swiss
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Pred. No. 0.0026;
4; Mismatches 153; Indels 174;
  of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                    PRT;
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EMBL outstation
             a collaboration
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InterPro; IPR001263; PI3 PI4
Pfam; PP00454; PI3 PI4 kInase;
Pfam; PP00613; PI3Ka; I.
Pfam; PP00792; PI3K C2; 1.
Pfam; PP00794; PI3K rbd; 1.
SMART; SM00142; PI3K rbd; 1.
SMART; SM00145; PI3Ka; 1.
SMART; SM00146; PI3Ka; 1.
SMART; SM00146; PI3Ka; 1.
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DOMAIN 166 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DictyDb; DD01100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. I
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InterPro; IPR000341; PI3K_ras_bind.
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                                     316 MS
266 NS
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FEDGGGGSSSSSGGRSNRRVRGGGSGQSGQIPRCQV------EGCGMDLTNAKG
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267
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20.5%;
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POLY-ASN
POLY-THR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 146; DB 1;
Pred. No. 0.0082;
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POLY-GLN
POLY-THR.
POLY-SER.
POLY-GLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A6C0333D4CDDEA03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1858;
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DROME

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RA Warn K. H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Demos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Podler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D.K., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Spler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
"The genome sequence of Drosophila melanogaster.",

"The genome sequence of Drosophila melanogaster.",

CC - Tarter J. S., Zhan M., Zhang G., Zhao Q., Zheng L.,
- Schence 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan, K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Wan, K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89057149; Propro A.E., Ong E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Knirps-related protein.
KNRL OR NROA2 OR CG4761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       steroid-receptor gene superfamily.";
Nature 336:493-496(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans R.M.
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                                                                                                                                                                        SIMILARITY: BELONGS TO
                                                                                                          gene model
                                                                                                                                                                                              SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                    NRO SUBFAMILY.
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                                                                                                                              Ref.2 sequence
                                                                                                        prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD
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., Margolis J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                      NUCLEAR HORMONE RECEPTOR FAMILY
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                                                                                                                                from that shown
long
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                 There are no restrictions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
               E78A DROME STANDARD; PRT; 865 AA.

P45447; O18395; O18396; Q9VP64;
O1-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Edysone-induced protein 78C (DR-78).
EIP78C OR NRIEI OR CG18023.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DOMAIN
SEQUENCE
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ZN FING
ZN FING
                                                                                                                                                                                 DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSFAC; T02773; -. FlyBase; FBgn0001323; knrl.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00105; zf-C4; 1.
PRINTS; PR00047; STROIDFINGER.
Probom; PD000035; Znf C4steroid;
SMART; SM00399; ZnF C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X14153; CAA32365.1; -. EMBL; AE003591; AAF51627.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00031; NUCLEAR RECEPTOR; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zinc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P20393; 1A6Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 VÉYGSHKHPVVASPSVSSPDSHNSDSSVEVSSVRGNPLLHLGGKSNSGGSSSGADGSH--
                                                                                                                                                                                                                                                                243 IGDSNCALSLLSNP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 RGGGSGQSGQIPRCQVEGCGMDLTN-------AKGY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEMGSNSGPGHGPGQAESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRV
                                                                                                                                                                                                                                                                                           GEDPRPSPG-QDNPIDL-SMKTTGSSLSSKSSSPEIEPETEISSDVEKNDTDDDDEDLKV
                                                                                                                                                                                                                                     TPEEEISVRETADPEIEEDHSSTTETAKTSIENTHNNNNSISNNNNNNNNNNNNN
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                                                                                                                                                                                                                                                                                                                                                                             A---SRYGRIAPSLYEN-----GDAGMNGSFLGNQEIGW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CRRRLAGH------SLSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YSRHRVCGVHSKTPK-----VTVAGIE-----QRFCQQCSRF--HQLPEFDLEKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGGGGGGGGGVTPGRPPQMRKDLSPFLPLPFPGLASMPVMPPPAFLPPSHLLFPGYHPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               finger; Developmental protein.

14 80 NUCLEAR R
IND 14 34 C4-TYPE.
ING 51 75 C4-TYPE.
ING 51 75 C4-TYPE.
IN 121 262 GLY-RICH.
IN 577 597 ASN-RICH.
                                                                                                                                                                                                                                                                                                                    MRRPVSSPSWQINPMNVFSQGSVGGGRTS-FSSPEI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSHHQ--GLLKPTPEQQQAAVAAAAVQHLFNSSGAGQRFAPGTSPFANHQQHHKEEDQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d and this statement is not removed. s requires a license agreement (See an email to license@isb-sib.ch).
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647
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262 G
597 P
68322 MW;
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21.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 125; DB
Pred. No. 0.08
42; Mismatches
                                                                                                                                                                                                                                                              E466FA081DAACDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA-binding; Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR-TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golale R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Button R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakkaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakkaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakkaroglu L.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Horil J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport I.B., Davies P.,
RA depablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA doston K., Doug I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA dolodson K., Doug I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Goldek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Degwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Hostin D., Houston K.A., Mixon K., Nusskern D.R., McCherson D.L.,
RA Mchulbov G., Milshina N.V., Mobarry C., Morris J., Moshredi A.,
RA Merkulbov G., Milshina N.V., Mobarry C., Morris J., Moshredi A.,
RA Melson D.R., Nelson K.A., Saunders R.D. C., Scheler F., Shen H.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Siger E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Siger E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Siger E., Sarquence of Drosophila melanogaster.";
RI H. Mang X., Smith H.O.,
RA Gibbs R.A., March J.S., Zhu X., Smith H.O.,
RA Gibbs R.A., Shorl P., Zhong W., Zhong X., Zhu 
                                                                                                                                                   Martin-Blanco E., Kornberg T.B., "DR-78, a novel Drosophila melanogaster genomic homologous to the DNA-binding domain of thyroid acid-vitamin D receptor subfamily.", Biochim. Biophys. Acta 1216:339-341(1993).

-I- FUNCTION: INDUCES THE EARLY LATE PUFF 78C WH-FORMATION AND DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., FUNCTION, AND STRAIN=Canton-S; TISSUE=Pupae; MEDLINE=97032934; PubMed=8878682;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, FUNCTION, AND INDUCTION STRAIN=Canton-S; TISSUE=Pupae, and Larva; MEDLINE=94006562; Pupmed=8402914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics 144:159-170(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stone
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94060116; PubMed=8241283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor superfamily.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 321-433 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Drosophila Eip78C gene is not vital but has a role in regulating
                                                                           SUBCELLULAR LOCATION: Nuclear (Probable).
ALTERNATIVE PRODUCTS: 2 isoforms; A/E78A (shown here) and B/E78B;
   may be produced by DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .R.H., Heimbeck G., Goddard C.M., Carpenter A.T.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          puffs.".
ed by alternative splicing.
STAGE: Isoform A is expressed only in mid-pupal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ISOFORM A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE SPLICING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                          WHICH
                                                                                                                                                                                                                                                                                                          DNA fragment highly hormone-retinoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nuclear hormone
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DOMAIN
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VARSPLIC
CONFLICT
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                                                                                                                                                                                                                                                                              DNA BIND
ZN_FING
ZN_FING
ZN_FING
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00047; STROIDFINGER.
PRODOM; PD000035; ZDf C4steroid; 1.
SMART; SM000430; HOLI; 1.
SMART; SM000430; MUCLEAR_RECEPTOR; 1.
PROSITE; P800031; NUCLEAR_RECEPTOR; 1.
Transcription regulation; DNA-binding; Nuclear protein; Metal-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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DOMAIN
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DOMAIN
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   SEQUENCE
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                          Zinc;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0004865; Eip78C.
InterPro; IPR000536; Mormone_rec_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAUTION: Ref.2 sequence differs from that shown frameshifts in positions 567 to 625.
CAUTION: Ref.3 sequence differs from that shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prepupae and immediately following isoform A in mid-pupae.
INDUCTION: Both isoforms require ecdysone for activity. Isoform
also requires ecdysone-induced proteins for maximal expression.
SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L; U01088; AAA19976.2; -.

; X98881; CAA67384.1; ALT_FRAME.

L; X98882; CAA67385.1; ALT_FRAME.

L; AE003593; AAF51692.1; ALT_SEQ.

L; X73045; CAA51523.1; -.

P; P20393; 1A6Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              stages, while isoform B is maximally expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NR1 SUBFAMILY
                                                                                                                                                                                                                                                                                                                ; Zinc-finger;
BIND 367
ING 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U01087; AAA19975.1;
U01088; AAA19976.2;
515
733
865
                                                39
75
321
325
430
433
                                                                                                                                             346
354
481
490
546
   B
  515 N
733 N
96024 MW;
                                                                                                                                                                                                                                                                                                                                          Alternative splicing
                                   ED -> DH (IN REF. 2; CAA67384).
MISSING (IN REF. 3).
QLQQQQQHQQQ -> SCNSSSSTSSR (IN REF. 4.
QO -> HE (IN REF. 2; CAA67384).
A -> V (IN REF. 4).
S -> K (IN REF. 4).
Q -> P (IN REF. 1; AAA19975 AND 2; CAA67384).
             MISSING
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POLY-ASN.
POLY-GLN.
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POLY-GLN.
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POLY-GLN.
                                                                                                                                   MISSING
                                                                                                                                                           POLY-GLN
   A52734720AFBA492 CRC64;
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             (IN REF. 2)
(IN REF. 1)
                                                                                                                                   (IN ISOFORM
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Query Match Best Local S Matches 78

Similarity

21.0%; 43;

Score 125; DB 1; Length 865; Pred. No. 0.11; 3; Mismatches 115; Indels 136;

Gaps

15;

Conservative

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RESULT 10
ST20_CANAL
ID ST20_C
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                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a copyright the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                MEDLINE=97075146; PubMed=8917572;
Kohler J.R., Fink G.R.;
Kohler J.R., Fink G.R.;
"Candida albicans strains heterozygous and homozygous for in mitogen-activated protein kinase signaling components in hyphal development.";
Proc. Natl. Acad. Sci. U.S.A. 93:13223-13228(1996).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: The SER/THR FAMILY OF PROTEIN
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01-NOV-1997 (Rel. 35,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q92212;
             Pfam; PF00069; pkinase;
Pfam; PF00786; PBD; 1.
                                   InterPro; IPR000719; Euk pkinase.
InterPro; IPR000095; PAKbox/Rhobndng.
InterPro; IPR0002290; Ser thr pkinase.
                                                                                      EMBL; U73457; AAB38875.1; -. HSSP; Q63450; 1A06.
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Saccharomycetales; mitosporic
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   PD000001;
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Euk_pkinase; 1.
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Last annotation update
ein kinase STE20 homol
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Best Local S
Matches 58
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01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-27 OR SNB1 OR YBL084C OR YBL0718.
16DC27 OR SNB1 OR YBL084C OR YBL0718.
18accharomyces cerevisiae (Baker's yeast).
18accharomyces (Baker's yeast).
18accharomycetales; Saccharomycetaceae; Saccharomycetes;
18accharomycetales; Saccharomycetaceae; Saccharomyces.
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DOMAIN
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SMART; SM00220; STK; 1.
SMART; SM00220; STK; 1.
PROSITE; PS50108; CRIB; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein_kinase; ATP-binding.
                                                                                                                                                                   STRAIN=S288c;
MEDLINE=96076635; PubMed=7502586;
Obermaier B., Gassenhuber J., Pir
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                                                                                                                                 Saccharomyces cerevisiae chromosome Yeast 11:1103-1112(1995).
                                                                                                                                                                                                                                                                                                                                                           P38042;
                                                                  Hieter P.A.;
                                                                            MEDLINE=92306611; PubMed=1819
Sikorski R.S., Michaud W.A.,
                                                                                           PARTIAL SEQUENCE FROM N.A., AND MUTAGENESIS MEDLINE=92306611; PubMed=1819514;
                                                                                                                                                Obermaier B., Gassenhuber J., Piravandi E., 
"Sequence analysis of a 78.6 kb segment of !
Saccharomyces cerevisiae chromosome II.";
                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=95009933; PubMed=7925276
              SUBUNITS
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                                    proteins as
Spring Harb.
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l Similarity 25.4%;
58; Conservative 2;
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E
                                       essential components of the yeast cell . Symp. Quant. Biol. 56:663-673(1991).
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PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.
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Pred. No. 0.19
23; Mismatches
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POLY-SER.
POLY-SER.
POLY-GLY.
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POLY-PRO.
                                                                              Wootton J.C., Boguski M.S.,
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EMBL; Z35845; CAA84905.1; -.
PIR; S45825; S45825.
SGD; S0000180; CDC27.
InterPro; IPR001440; TPR.
Pfam; PF00515; TPR; 8.
SMART; SM00028; TPR; 5.
Cell division; Cell cycle; Mitosis; R
                                    DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lamb J.K., Cdc23p and C. "Cdc16p, Cdc23p and C. 13:4321-4328 (1994)
EMBO J. 13:4321-4328 (1994)
EMBO J. TAMTON: EXECUTES EST
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MUTAGEN
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Drosophila melanogaster (Pruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE CDC27/NU-!- SIMILARITY: CONTAINS 8 TPR REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: CDC16, CDC23 AND CDC27
-!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                         328
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                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: EXECUTES ESSENTIAL MITOTIC METAPHASE/ANAPHASE TRANSITION.
                                                                                                                                                                                                                                                                                                                                          HNNNAASSFPS--TSLSHFEPRSQPSLYSKTNKNGNNNINNNVNTLFQSSNS------
                                                                                                                                                                                                              PMTVTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSG 336
                                                                                                                                                                                                                                                                                                                PVSSPSWQINPMNVFSQGSVGGGRTSFSSPEIMDTKLESYKGIGD------SNCALSLL
                                                                                                                                                                                                                                         SPSSKQPTISSLAKVYNRNKLLTTPPSKLLNNDRNHQNNNNNNNNNNNNNNNN
                                                                                                                                                                                                                                                                                        PPSTSASSFSSIQHFSRSQQQQANTSIRTCQNKNTQTPKNPAINSKTSSALPNNISMNLV
                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Michaud W.A., Sikorski R.S., Hieter P.A.; Cdc23p and Cdc27p form a complex essential for mitosis.";
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BELONGS TO THE CDC27/NUC2 FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
505
573
607
641
675
                                                                                                                                                                                                                                                                                                                                                                                                                                            85436 MW;
                                                                                                                                                                                                                                                                                                                                                                                                      20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%;
                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                      ----NNNNNNNNI INKTTFKTPRNLYSSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitosis;
                                                                                                                                                                                                                                                               -----NPHQPHDNNNNNNNNNNNNNNTWRASSGFG
                                                                                                                                                                                                                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 123.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPR 8.
ASN-RICH.
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TPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                          8612EA4504327A02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; TPR repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORMS A MACROMOLECULAR COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
Pancrustacea; Hexapoda;
Diptera; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                          76; Indels
                                                             (GATA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEAR
                                                                                                                                                                                                                                                                                                                                                                                          79;
                                                              factor-B)
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Best Local
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"A Drosophila GATA family member that binds to Adh regulatory sequences is expressed in the developing fat body.";

Development 119:623-633 (1993).

-!- FUNCTION: MAY FUNCTION AS A TRANSCRIPTIONAL ACTIVATOR PROTEIN AND MAY PLAY A KEY ROLE IN THE ORGANOGENESIS OF THE FAT BODY. BINDS A SEQUENCE ELEMENT (5'-[TA]GATAA-3') FOUND IN THE LARVAL PROMOTERS OF ALL KNOWN ALCOHOL DEHYDROCENASE (ADH) GENES. ACTS AS A HOMEOTIC GENE DOWNSTREAM OF THE TERMINAL GAP GENE HKB TO PROMOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear
ZN_FING
                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00344; GATA_ZN_FINGER_1; PROSITE; PS50114; GATA_ZN_FINGER_2; Transcription regulation; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0003507; EInterPro; IPR000679; ZI
Pfam; PF00320; GATA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X76217; CAA53807.1; -. HSSP; P17678; IGAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94244465; PubMed=8187633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=7227;
                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                     239
    66 GOSGQIPRCQVEGCGMDLTNAKGYYSRHRV---CG----VHSKTPKVTVAGIEQRFCQQC
                                                                                                16 AESGGSSTESSSFSGGLMFGQKIYFEDGGGGSGSSSSGGRSNRRVRGG-----GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 GATA-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOUND IN BOTH THE ENDODERMAL AND MESODERMAL GERM LAYERS AND FOR BRIEF PERIOD DURING GASTRULATION IT IS EXPRESSED IN THE AMNIOSEROSA. DURING GERM BAND RETRACTION IT BECOMES RESTRICTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Nuclear.

DEVELOPMENTAL STAGE: INITIALLY OBSERVED IN THE ANALGEN OF THE ANTERIOR AND POSTERIOR MIDGUT AND THE CEPHALIC MESODERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MORPHOGENESIS AND DIFFERENTIATION OF ANTERIOR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; PR00619; GATAZNFINGER.
SM00401; ZnF_GATA; 1.
                                                                                                                                              75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                       779 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                          319
62
81
132
206
439
                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  257
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POLY-ASN.
POLY-ASN.
POLY-SER.
POLY-ALA.
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                                                                                                                                                                 Score 123.5; I
Pred. No. 0.13;
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                                                                                                                                                                                                                                                               POLY-GLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-GLY
                                                                                                                                                                                                                                          7D4AD12A241E986D CRC64;
                                                                                                                                              Mismatches
                                                     GGGRSKANTSGAASSYSCPGSNATSAATSAVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              There are no restrictions of as its content is in
                                                                                                                                                                                       DB 1;
                                                                                                                                              122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                              Indels
                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zinc-finger;
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288 GTAATAATTLDE--HVSRANSRRLSASKRAGLSCSNCHTTHTSLWRRNPAG--EPVCNAC

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P49657;
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tejedor F., Zhu K.R., Kaltenbach E., Ackermann A., Baumann A., Canal I., Heisenberg M., Fischbach K.F., Pongs O.; "Minibrain: a new protein kinase family involved in postembryonic neurogenesis in Drosophila."; Neuron 14:287-301(1995).

-I- FUNCTION: ROLE IN THE SPECIFIC CONTROL OF PROPER PROLIFERATION OF OPTIC LOBE NEURONAL PROGENY. MUTANTS ARE CHARACTERIZED BY A SPECIFIC AND MARKED SIZE REDUCTION OF THE OPTIC LOBES AND CENTRAL BRAIN HEMISPHERES BUT NO MAJOR ALTERATION IN NEURONAL ARCHITECTURE
                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MNP.
                                 EMBL; X70794; CAA50065.1; -.
EMBL; X70798; CAA50068.1; -.
EMBL; X70799; CAA50069.1; -.
HSSP; P24941; 1BUH.
                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                      the
                                                                                                                                                                                                                                                          +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Berlin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Inaseta; Pterygota; Neopteera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95161060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
                                                                                                                                                                                                                                                                                      NEUROPIL AND THE OUTER PROLIFERATION CENTER OF THE OPTIC LITHIRD INSTAR LARVAE.

DEVELOPMENTAL STAGE: THE FORMS A AND C ARE PRESENT MAINLY EMBRYOS AND PUPAE. BY CONTRAST, FORM B APPEARS TO BE EXPREMOST MARKEDLY IN THIRD INSTAR LARVAE AND PUPAE.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINAS
                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: IN VENTRAL HERVE CORD AND SUPRAOESOPHAGEAL GANGLION OF EMBRYOS. IS MOST PROMINENT IN THE MUSHROOM BODY
                                                                                                                                                                                      European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAN BE FOUND.
                                                                                                                                                                                                                                                                            MNB/DYRK SUBFAMILY
                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration - sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACSTHPAHPLHLQHPSPTHQLHNNNNNNNSSLFNNNNNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSPHSMGSTSL-SPSAMSHQHQTHPHQQQQQQLCSGWTCRPTQTTKCRRSTCSSISSSNR 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNCHNVGVVLDSSQMDVNDDMKPQLDLKPYNSYSSQPQQQLPQYQQQQQLVMADQHSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNGSFLG-----NQEIGWPSSRTLDTRVMRRPVSSPSWQI-----NPMNVFSQGSVGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S---RFHQLPE-FDLEKRSCRRRLAGHNERRRKPQPASLSVLASRYGRIAPSLYENGDAG
IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -GRTSFSSPEIMDTKLESY---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 33,
(Rel. 33,
(Rel. 40,
                                                                                                                                                                                                                                                          IT IS UNCERTAIN WHETHER MET-1 OR MET-16 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Nuclear (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSLLSNPHQPHDNNNNNN----NNNNNNNNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=7857639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
ein kinase minibrain (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         843
                                                                                                                                       (See
                                                                                                                                                                   There are no restrictions in as its content is in
                                                                                                                                     http://www.isb-sib.ch/announce/
                                                                                                                                                   Usage
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                                                 Q24432; Q27917; Q9W4K5;
01-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Optomotor-blind protein (Lethal(1)optomotor-blind)
                                                                                                     BMO
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BINDING
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ProDom; PD000001; Euk pkinase; 1.

SMART; SM00220; S TKG; 1.

PROSITE; PS00107; PROTEIN KINASE ATF; 1.

PROSITE; PS00108; PROTEIN KINASE ST; 1.
           Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Man
                               protein).
BI OR OMB OR CG3578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT
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Transferase; Serine/threonine-protein kinase; ATP-bin
Nuclear protein; Alternative splicing; Developmental
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                                                                                                                                                                                               HHSTNSLGSLNHISPGSTGCHNNNSNSSNNNT-RHSRLYGSNMVNMVGHHNSGSSNNHNS
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 Pterygota;
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  Neoptera;
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 0.14;
1; Mismatches
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POLY-PRO.
POLY-SER.
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  Endopterygota;
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           Mandibulata;
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(IN ISOFORM B)
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Pancrustacea;
Diptera; Brach
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           Hexapoda;
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RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D.D., Celniker S.E., Hich R.A., Sahburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barlew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Barli J.F., Apbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Dovies P.,
RA Borkova D., Botchan M.R., Bouck J., Brokatesin P., Brottier R.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dovies P.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dukov B.C., Dunn P.,
RA Goldek A., Gang P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L.,
RA Rahert K., Renington K., Saunders R., D.C., Scheeler F., Shen H.,
RA Sylress R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Glibs R.A., Wyers E.W., Zhong W., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Zhong W., Zhan G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Zhong W., Shushi M.O., Zhang G., Zhao Q., Zheng L.,
Ra Gibbs R.A., Myers E.W., Schoel R., Zhu S., Zhu X., Smith H.O.,
Ra Gibbs R.A., Myers E.W., Schoel R., Zhu S., Zhu X., Smith H.O.,
Ra Challey R., Shu B., Shu S., Shu M., Shu S., Shu M., Shu S., Shu M., Shu S., Shu N., Shu S., Shu 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93261414; PubMed=8492800; Poeck B., Balles J., Pflugfelder G.O.; Prock B., Balles J., Prock B., Prock 
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STRAIN=Oregon-R; TISSUE=Embryo;
MEDLINE=92159016; PubMed=1741374;
Pflugfelder G.O., Roth H., Poeck |
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NCBI_TaxID=7227;
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PUNCTION: ESSENTIAL PROTEIN THAT MAY FUNCTION AS A TRANSCRIPTION REGULATOR. FLIES WITH L(1)OMB MUTATIONS SHOW SEVERE MALDEVELOPMENT OF THE OPTIC LOBES, REDUCTION IN WING SIZE AND AN INCREASED ABDOMINAL PICHENTATION. THEY DIE DURING THE PUPAL STAGE.

SUBCELLULAR LOCATION: Nuclear (Potential).

TISSUE SPECIFICITY: IN THIRD-INGTAR LARVAE IT IS FOUND IN THE BRAIN REGION THAT WILL DEVELOP INTO OPTIC LOBES AND MORE WEAKLY IN THE THORACIC PART OF THE VENTRAL GANGLION.

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Acad. Sci. U.S.A. 89:1199-1203 (1992).
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B A E

YK76 YEAST P36168;

STANDARD;

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01-JUN-1994 (Rel. 29, Created)

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EMBL; S61732; AAB26697.1; -
EMBL; S61727; AAB26697.1; JOINED
EMBL; S61729; AAB26697.1; JOINED
EMBL; S61744; AAB26699.1; -
EMBL; S61744; AAB26699.1; -
EMBL; S61743; AAB26699.1; JOINED
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DOMAIN
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PROSITE; PS01264; TBOX_2; 1.
PROSITE; PS50252; TBOX_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP;
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                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               DNA-binding; Nuclear DOMAIN 51 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00937; TBOX. SMART; SM00425; TBOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0000179; b:
InterPro; IPR001699; TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M81796; AAA28736.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute.
                                                                                                                                                                                    173
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                         194
                                                            348
                                                                                 149
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                                                                                                                                            228
                                                                                                                                                               48
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                                                                                                                                                                                    AGMNGSFLGNQEIGWPSSRTLDTRVMRRPVSSPSWQINPMNVFSQGSVGGG-----RTSF 227
                                         PSHH-----PTAAHHS
                                                           --HHQSRRQYMEDENTRAYDSSSHHT
                                                                               LSTTEEPPSPAG---TPPPTIV----GLPPI--
                                                                                                   VTMAQPPPAPSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMGEFELSDH
                                                                                                                       SSPEIMDTKLESYKGIGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPMT
                                                                                                                                                                 AGSNNNNSGNTNSGNNNSNSNN-----NTNSNTNNTNNLVAVSPTGGGAQLSPQSNH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00907;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S61955;
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                         216
511
823
976
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104
179
229
238
238
332
574
607
823
910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; T-box; 1.
37; TROY
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                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                               103992 MW;
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                                                                                                                                                                                                       Score 123; DB
Pred. No. 0.18
33; Mismatches
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F -> L (IN REF.
A -> P (IN REF.
F -> L (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                ASN-RICH.
POLY-THR.
POLY-SER.
POLY-GLN.
                                                                                                                                                                                                                                               MISSING (IN REF. 1).
MISSING (IN REF. 1).
v; 032B7A4471743FC9
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                                        204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There
                                                                                                                                                                                                                          DB 1; Length 988;
                                                                                 --- PPPNNNSSSSSSNNSASAAAH
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                                                                                 193
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Best Local Similarity 22.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-843 FROM N.A.
Baladron V., Ballesta J.P.G., Bou G., del Rey F., Estebi
Baladron V.J., Gonzalez A.,
Garcia-Cantalejo J.M., Garcia-Ramirez J.J., Gonzalez A.,
Revuelta J.L., Santos M.A.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).

Sukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaillon L. Dujon B.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
SIMILARITY: STRONG, TO YEAST YILLISIC. ALSO TO THE N-TERMINAL OF YEAST ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL 1 (ALD1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical 137.5 YKR096W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Hypothetical 137.5 kDa protein in MPL1-PPC1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z28321; CAA82176.1; -. PIR; S38174; S38174. SGD; S0001804; YKR096W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; ATP-binding.
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                                                                                                                                                                                                                                                                                                                               142
                                                                         245
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                                                                                                                                                                                                                                                                                                                                                                                                   82 DITNAKGYYSRHRVCGVHSKTPKVTVAGIEQRFCQQCSRFHQLPEFDLEKRSCRRRLAGH 141
                                                                                                                                                                                                                                                                                           SEKNPSPRYVSSSKRALKRENSVGITQSSALISKSFSENG-----GSIAHEK---W---- 152
                                                                                                                                                                                                                                                                                                                             NERRRKPOPASISVLASR------YGRIAPSLYENGDAGMNGSFLGNQEIGWPSSR 191
                                                                                                                                                                                                                                                                                                                                                                 DINSSKRRISRPRFSDIEGK------NNDHTYPE-----RTTVKE 104
                                                                                                         AQPPPAPSQHQYLNPPWVFKDNDNDMSPVLNLGRYTEPDNCQISSGTAMG 340
                                                                                                                                                                  ----TKLESYKGIGDSNCALSLLSNPHQPHDNNNNNNNNNNNNNNNTWRASSGFGPMTVTM 290
                                                                                                                                                                                                                     -----SPENMIKPLNV-SQNSLAFVDAGSDEQSKSEIVGGFQRKSNNSQEIND
                                                                                                                                                                                                                                                       TLDTRVMRRPVSSPSWQINPMNVFSQGS-------VGG-GRTSFSSPEIMD 234
                                                                                                                                             KDNSARDQDFNNSGNNN-----NNNHSSNNNDNNNNNNDDNNNNNNSNS----
                                                                                                                                                                                                                                                                                                                                                                                                                                           65
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465 4
1195 AA;
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472
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                 2003, 13:53:28
                                                                         -RDNNNNSD----DSNEREENDSCKPASNKRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 122.5; DB 1; Length 1195; Pred. No. 0.24; Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL)
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Gonzalez A., Jimenez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                       75; Indels 119;
                                                                         272
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